

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_p1ue\_p2n model

Run on: March 22, 2005, 05:20:43 | Search time 564 Seconds  
(without alignments)  
2248.292 Million cell updates/sec

Title: US-09-525-867-1  
Perfect score: 1118  
Sequence: 1 MAVLSAPQGLKGFRLGLRSS.....ILQQRKIKRRRQIWR 213

Scoring table:  
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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 5544816 seqs, 2976611598 residues  
Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -WATRIE=1locum62  
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Database :

Published Applications NA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1118	100.0	772	US-10-037-270-670	Sequence 670, App
2	1118	100.0	772	US-10-117-722-670	Sequence 670, App
3	965	86.3	2818	US-10-104-047-625	Sequence 625, App
4	891.5	79.7	3089	US-10-104-047-914	Sequence 914, App
5	863	77.2	3050	US-10-104-047-262	Sequence 262, App
6	743	66.5	797	US-10-767-701-19893	Sequence 19893, A
7	740.5	66.2	1092	US-10-767-701-14502	Sequence 14502, A
8	737.5	66.0	886	US-10-425-114-16284	Sequence 16284, A
9	737.5	66.0	949	US-10-425-114-6711	Sequence 6711, App
10	737.5	66.0	1394	US-10-425-115-3877	Sequence 3877, App
11	735.5	65.8	1840	US-10-425-115-3875	Sequence 3875, App
12	731.5	65.4	753	US-10-320-797-2049	Sequence 2049, App
13	729	65.2	1356	US-10-424-599-6216	Sequence 6216, App
14	726.5	65.0	863	US-10-425-114-36399	Sequence 36399, A
15	725	64.8	1532	US-10-424-599-6217	Sequence 6217, App
16	723.5	64.7	1142	US-10-437-963-92496	Sequence 92496, A
17	702	62.4	735	US-10-128-714-7030	Sequence 7030, App
18	698	62.4	672	US-10-032-585-6755	Sequence 6755, App
19	676	60.5	466	US-10-152-319A-195	Sequence 195, App
20	670.5	60.0	570	US-10-128-714-2030	Sequence 2030, App
21	654	58.5	2731748	US-10-297-465A-1	Sequence 1, Appl
22	638.5	57.1	596	US-10-128-714-1030	Sequence 1030, App
23	638.5	57.1	873	US-10-128-714-6030	Sequence 6030, App
24	638.5	57.1	2596	US-10-128-714-30	Sequence 30, Appl
25	638.5	57.1	2873	US-10-128-714-5030	Sequence 5030, App
26	619	55.4	966	US-10-320-797-1049	Sequence 1049, App
27	619	55.4	2420	US-10-320-797-49	Sequence 49, Appl
28	618	55.3	344	US-10-775-169-55	Sequence 55, Appl
29	496.5	44.4	480	US-10-335-977-1662	Sequence 1662, App
30	458.5	41.0	9025608	US-10-156-761-1	Sequence 1, Appl
31	453.5	40.6	609	US-10-156-761-4866	Sequence 4866, Appl
32	441	39.4	274	US-10-425-115-158531	Sequence 158531, App
33	441	39.4	552	US-10-156-761-4822	Sequence 4822, App
34	433.5	38.8	3148	US-10-424-599-30088	Sequence 30088, A
35	431.5	38.6	58909	US-10-672-787-30	Sequence 30, Appl
36	429.5	38.4	4352	US-10-425-115-37889	Sequence 37889, A
37	428	38.3	640681	US-09-790-988-1	Sequence 1, Appl
38	418	37.4	446	US-09-991-936-1794	Sequence 1794, App
39	411	36.8	789	US-09-759-143-32	Sequence 32, Appl
40	411	36.8	789	US-09-780-669-32	Sequence 32, Appl
41	411	36.8	789	US-09-030-606-32	Sequence 32, Appl
42	411	36.8	789	US-09-822-827-32	Sequence 32, Appl
43	411	36.8	789	US-09-115-453-32	Sequence 32, Appl
44	411	36.8	789	US-09-232-880-32	Sequence 32, Appl
45	411	36.8	789	US-09-895-793-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1  
US-10-037-270-670 Application US/10037270  
; Sequence 670, Application No. US20030104529A1  
; Publication No. US20030104529A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyun  
; APPLICANT: Chen, Ruihong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehtman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yunqing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei



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QY 141 MeProGluProArgTYrValValSerMetGlySerCysAlaAenglyGlyTYrTYr 160
Db 444 ATGCCGGAGCCGCTACGTGCTCCATGGAGAGCTGCGCAACGAGAGGCTACTAC 503
QY 161 HistYSerTYrSerValValArgGlyCysAspArgIleValProValAspIleTYrIle 180
Db 504 CACTATTCCTACTCGGTGTAGGGGCTGCACCGCATCGGCCGTGGACATCTACATC 563
QY 181 ProGlyCysProProThraAlaGluAlaLeuLeuTYrGlyIleLeuGlnLeuGlnArgIys 200
Db 564 CCAGCTGCTCCACCTACCGCCGAGGCTCTGCTTACCGCATCTGACATCTGACAGGAAG 623
QY 201 IleYsaArgGluArgArgLeuGlnIleTYrTYrArgArg 213
Db 624 ATCAAGCGGAGCGGAGGCTGACATCTGTACCGCAGG 662

RESULT 3
US-10-104-047-625
; Sequence 625, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 625
; LENGTH: 2818
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-625

Alignment Scores:
Pred. No.: 3,16e-114 Length: 2818
Score: 965.00 Matches: 186
Percent Similarity: 96.88% Conservative: 0
Best Local Similarity: 96.88% Mismatches: 2
Query Match: 86.31% Indels: 4
DB: 17 Gaps: 1

US-09-525-867-1 (1-213) x US-10-104-047-625 (1-2818)
QY 1 MetAlaValLeuSerAlaProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSerSer 20
Db 24 ATGCGGCTGCTGTAGCTCTGCGCTGCGCGCTTCCGATCTT3GTCTGCGCTCCAGC 83
QY 21 ValGlyProAlaValAlaGlnArgGlyValHisGlnSerValAlaThrAspGlyProSer 40
Db 84 GTGGGCCCCGCTGTGACGACGAGGTGTCCATCAGACGCTGACCGCATGGGCCCAAGC 143
QY 41 SerThrGlnProAlaLeuProLyAlaArgAlaValAlaProLySProSerSerArgGly 60
Db 144 AGCACCCAGCTGCTGCTGCCAAGGCCAGACCGGTGCTCCCAACCAAGACGCCGGGC 203
QY 61 GluTYrValValAlaValSLeuAspAspLeuValAsnTPAlaArgArgSerSerLeuTYr 80
Db 204 GAGATATGTGTGGCCAGAGCTGATGACCTCGTCAACTGGGCCCGCCGAGATTCTCTGG 263
QY 81 ProMetThrPheGlyLeuAlaCysCysAlaValAlaGlnMetMetHisMetAlaProArg 100
Db 264 CCCATGACCTTGGCTGGCTGCTGCGCCGTGGAGATGATGACATGGACGACCCCGC 323
QY 101 TyrAspMetAspArgPheGlyValValPheArgAlaSerProArgGlnSerAspValMet 120
Db 324 TAGACATGACACCGCTTTGGGTGTCTTCCGCGCAGCCCGCTCCAGTCCGATATG 383
QY 121 IleValAlaGlyTYrLeuThrAsnLyMetAlaProAlaLeuValGlyValTYrAspGln 140
Db 384 ATCTGGCCGCGACATCAACCAAGATGGCCCGAGCGCTTGTGCAAGTCTACGACACAG 443
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QY 141 MeProGluProArgTYrValValSerMetGlySerCysAlaAenglyGlyTYrTYr 160
Db 444 ATGCCGGAGCCGCTACGTGCTCCATGGAGAGCTGCGCAACGAGAGGCTACTAC 503
QY 161 HistYSerTYrSerValValArgGlyCysAspArgIleValProValAspIleTYrIle 180
Db 504 CACTATTCCTACTCGGTGTAGGGGCTGCACCGCATCGGCCGTGGACATCTACATC 563
QY 181 ProGly-----CysProProThraAlaGlu 188
Db 564 CCAGTATGGCCGGGAGCCGACCGCACCGCAGAGGAG 599

RESULT 4
US-10-104-047-914
; Sequence 914, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 914
; LENGTH: 3089
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-914

Alignment Scores:
Pred. No.: 1.23e-104 Length: 3089
Score: 891.50 Matches: 185
Percent Similarity: 68.01% Conservative: 0
Best Local Similarity: 79.74% Mismatches: 3
Query Match: 17 Indels: 85
DB: 17 Gaps: 2

US-09-525-867-1 (1-213) x US-10-104-047-914 (1-3089)
QY 1 MetAlaValLeuSerAlaProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSerSer 20
Db 53 ATGCGGCTGCTGTAGCTCTGCGCTGCGCGCTTCCGATCTTGGTCTGCGCTCCAGC 112
QY 21 ValGlyProAlaValAlaGlnArgGlyValHisGlnSerValAlaThrAspGlyProSer 40
Db 113 GTGGGCCCCGCTGTGACGACGAGGTGTCCATCAGACGCTGACCGCATGGGCCCAAG- 171
QY 40 ----- 40
Db 172 CAGGTGAAGCTGCTTGTGGGGAGGTGTACCCCTGCGCCGACCCCATCCCTTCTCCT 231
QY 40 ----- 40
Db 232 TATTTTCTGATCAGTCCCGACGACCTAGAGTGCATGATGGGCGAGGAGGGGTAC 291
QY 40 ----- 40
Db 292 ACATCCAGTCCCTGACCTCATGTGGGTCCAGGCTCTGGCAGGGCGGTGGGGCTGCG 351
QY 40 ----- 40
Db 352 ATCCGCTCTGGGAAGACCTGCTGGCTGACGCTCTGTGCTGTGTCTGTGCTC 411
QY 41 SerThrGlnProAlaLeuProLyAlaArgAlaValAlaProLySProSerSerArgGly 60
Db 412 AGCACCCAGCTGCTGCTGCCAAGGCCAGACCGGTGCTCCCAACCAAGACGCCGGGC 471
QY 61 GluTYrValValAlaValSLeuAspAspLeuValAsnTPAlaArgArgSerSerLeuTYr 80
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RESULT 5
US-10-104-047-262
? Sequence 262, Application US/10104047
? Publication No. US20030236392A1
? GENERAL INFORMATION:
? APPLICANT: HELIX RESEARCH INSTITUTE
? TITLE OF INVENTION:
? FILE REFERENCE: NO. US20030236392A1e1 full length cDNA
? CURRENT APPLICATION NUMBER: H1-40105
? CURRENT FILING DATE: US/10/104,047
? PRIOR APPLICATION NUMBER: 2002-03-25
? PRIOR FILING DATE:
? NUMBER OF SEQ ID NOS: 4096
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 262
? LENGTH: 3050
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-104-047-262

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Alignment Scores:	
Pred. No.:	6.05e-101
Score:	863.00
Percent Similarity:	95.40%
Best Local Similarity:	95.40%
Query Match:	17.19%
DB:	17
Gaps:	1
Length:	3050
Matches:	166
Conservative:	0
Mismatches:	4
Indels:	1

US-10-104-047-262 (1-3050)

QY	15	SeSeSeValGjYProAlaValAGlnAlaArgGjYValHisGlnSeSeSeValAlaItrnAspGjY	38
Db	307	TCcAcCGTGGCCGTGGCTGTGGcAGGAcCAGAGTTCATcAGAcCGTGGCCACCATGGCC	36
QY	39	ProSeSeSerTrnGlnPProAlaLeuPolYValAlaArgAlaValAlaIPolYsPProSeSer	58
Db	367	CCAcGACAGAcCCcAGCCCTGGCCCTGGCCcCAGAGGcCAGAcCGTGGCTCCcAAACCCcAGAcGC	42
QY	59	ArgGjYglnTrYValValAlaIstLeuSpsAspLeuValIseTrpAlaArgTrSeSer	78
Db	427	CGGGcCAGATnGTGGTGGCCAcGTGAATAcCTTCGTCAAcGTGGCCCGCGAGTTC	48
QY	79	LeuTrpPromeTrhPheGjYLeuAlaCyCyAlaValAlaGluMetMetHisMetAla	98
Db	487	CTGTGGCCcATGAcCTTCGTGGcCTGTGGCTGTGGCCCGCTGTGAATGATGAcCATGTGGAcCA	546
QY	99	ProArgTrYAspMetcAspArgPheGjYValValPheArgAlaSeTrpArgGlnSeTrasp	118

Db	547	CCCCGCTACGACATGAGCCGCTTTGGCGTGGCTTCCGGCCAGCCGGCCGACCCCGAC	606
Qy	119	ValMetIleValAlaaglyThrIleuThrAsnIleAsnMetAlaProIleAlaMetArgIleValTyr	138
Db	607	GTCATGATCGTGGCGGCGACACTCACCACCAAGATGAGCCCGAGCGCTTCCGACGGCTTAC	666
Qy	139	AspIleMetProGluIleProArgTyrValIleSerMetGlySerCysValAlaAsnGlyIcylGly	158
Db	667	GACCAAGTCCGGAGAGCGCGCTACCGTGGCTTCCATGGGGAGCGTCCGCCACGAGAGAGCC	726
Qy	159	TyrThrHisTyrSerTyrSerValValArgIleCysAspArgIleValProValIlePhe	178
Db	727	TACTACCACTAATTCATCTACTCGGTGTGTAGGGGGTGCACACCGCATCTGCTGGCGTCACTC	786
Qy	179	TyrIleProGly-----CysProProThrValIadju	188
Db	787	TACATCCACGATGAGGCGCGGAGCCGACCCGCCACGAGGAGG	828

US-10-767-701-19893  
; Sequence 19893, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION.

```

1  APPLICANT: Kovalic, David K.
2  APPLICANT: Zhou, Yihua
3  APPLICANT: Cao, Yongwei
4  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
5  TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
6  FILE REFERENCE: 38-21(5)355B
7  CURRENT APPLICATION NUMBER: US/10/767,701
8  CURRENT FILING DATE: 2004-01-29
9  NUMBER OF SEQ ID NOS: 63128
10 SEQ ID NO 19893

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Alignment Scores:	
Read No.:	3,65e+06
Score:	743.00
Percent Similarity:	72.53%
Best Local Similarity:	61.80%
Conservative Match:	66.46%
B:	18
Length:	
Matches:	
Conservative:	
Mismatches:	
Indels:	
Gaps:	

US-10-767-701-19893 (1-797)

1 MetAlaValLeuSerAlaProGlyLeuAngGlyPheArgIleLeuGlyLeuArgSer 20  
2     |||||.....  
3     ATGTCGTATATACACCAAGSTCTCCGAAC-----GGGCTCCAGAGCTCG 81  
4     21 -----ValGlyProAlaValAlaIle 27  
5     82 TCTTCTCTCCAGACCAACCTTTCATCGACAGCACTCTCCACATCGGCCATCGCT 141  
6     28 ArgGlyValHisGlnSerValAlaThrAspGlyProSerSerHisGlnProAlaLeuPro 47  
7     142 GGTAAACCAAGATTCTTCCATTAGTATCGGACCCATCTCCATCAAGATCAACATCA 201  
8     48 LysAlaArgAla-----ValAlaProLysProSerSerArgGly 60  
9     202 ACTAGAACACGCTCAGAAAGGTCAAAACCAACTTCTCTGGAAATCTCCAGCAAGCGGCGCT 261  
10    61 GlnTyrValValAlaIleLeuAspAspLeuValAsnTyrAlaArgArgSerSerLeuTyr 80  
11       |||||.....  
12       .....

Db 262 GAATATGCTTGTGCACTCTTGATAAATGGCTCAATTGGGCTAGACAAAGTTTCGATGTGG 321  
Qy 81 PrometThPhegIyLeuAlaCyCyseAlaValaGluMetMeChIsmetAlaAlaProArg 100  
Db 322 CCGATGACTTTCGGTTGGCTTGTGGCCCGTAGAGATGATGCACATGCTGCTGCTAGA 381  
Qy 101 TyrAspMetAspArgPheGlyValaValaPheArgAlaSerProArgGlnSerAspValMet 120  
Db 382 TATGACCAAGATTCAGTTGGTGGTGTGTGTTCCGAGCCAGTCCCTCGACAAAGATATCATG 441  
Qy 121 IleValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysValaTyrAspGln 140  
Db 442 ATATAGCCCGGTATCATTTGACCAACAAAGATGGCGCAGCTCTTGAAGGTTACAGATCAA 501  
Qy 141 MetProGluProArgTyrValaValaSerMetGlySerCyseAlaAsnGlyGlyTyrTyr 160  
Db 502 ATGGCAAGAACCAAGATGGGTCAITTCATGGGTTCTTGTGCCAAGGAGGAGTTACTAC 561  
Qy 161 HisTyrSerTyrSerValaValaArgGlyCyseAspArgIleValaProValaAspIleTyrIle 180  
Db 562 CACTACTGCTACTCTGTTGTGAGAGTTGTGACCGTATAGTTCCGCTGACATTTAGCTC 621  
Qy 181 ProGlyCyseProProthrmAlaGluAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArgLys 200  
Db 622 CCAGATGTCCACCCACATCGCCAGGCTCTGTTGTACGGTATGCTTGCCTTCAGCGAAG 681  
Qy 201 IleLysArgGluArgArgLeuGlnIleTyrTyrArgArg 213  
Db 682 ATGGCAAGAACCAAGACGCGCGCTCATGTGTACAGAA 720

## RESULT 7

US-10-767-701-14502  
; Sequence 14502, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(5353)B  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 14502  
; LENGTH: 1092  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28WAY03-CLUS4585\_1  
US-10-767-701-14502

## Alignment Scores:

Pred. No.:	1.18e-85	Length:	1092
Score:	740.50	Matches:	144
Percent Similarity:	75.12%	Conservative:	19
Best Local Similarity:	66.36%	Mismatches:	46
Query Match:	66.23%	Indels:	8
DB:	18	Gaps:	2

US-09-525-867-1 (1-213) x US-10-767-701-14502 (1-1092)

Qy 4 LeuSerAlaProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSerSerValaGlyPro 23  
Db 73 CTTCCACGCCCTCTCCACAGAGGTGAGAAACCTTAGACCCAGACCATGAGCGCTGCTCC 132  
Qy 24 AlaValGlnAlaArgGlyVala-----HisGlnSerValaAlaThrAs 37  
Db 133 GCGACGCGCGGCGGCTCTCTCCATCCGCGGCGCTACTCCGCGCGCGCTGCG 192  
Qy 37 pGlyProSerSerThrmGlnProAlaLeuProLysAlaArgAlaValaLysProSe 57  
Db 193 GGGGCGCTCTGACGTCCAGCG---CATATACGGGGCGCGCCCGCGCGAGATGTC 249

Qy 57 rSerArgGlyGlyTyrValaValaLysLeuAspAspLeuValaSerTrpAlaArgSe 77  
Db 250 GAACAGCGCCAGATTCGTGTGCTCCACAGTCGACGACTGATGACATGGCGGCTTAGCG 309  
Qy 77 rSerLeuTrpProMetThrPheGlyLeuAlaCyCyseAlaValaGluMetMeChIsmetAl 97  
Db 310 CTCGATCGGCGCATGACCTTCGGGCTCGCTGCGCGGTGAGATGATGACACGCCGG 369  
Qy 97 aAlaProArgTyrTrpMetAspArgPheGlyValaValaPheArgAlaSerProArgLys 117  
Db 370 CGCTCCCGCTACGACTTCGACCGGTTCCGCTATCTTCGCTCCGCGCAGCTC 429  
Qy 117 rAspValMetIleValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysVa 137  
Db 430 CGATTCGATGATCTCCCGGACAGCTCACCAACAAGATGCTCAGCCCTCCGCAAGT 489  
Qy 137 lTyrAspGlnMetProGluProArgTyrValaValaSerMetGlySerCyseAlaAsnGly 157  
Db 490 TTATGACCAAAATGCGCTAGCGCTGATTTCAATGGGCAAGCTGTGCCAACGGTGG 549  
Qy 157 yGlyTyrTyrHisTyrSerTyrSerValaValaArgGlyCyseAspArgIleValaProVala 177  
Db 550 TGTATCTACCATTACTCTGTTGTGACGTGAGATGACCGTATAGTCCCTGTGGA 609  
Qy 177 pIleTyrIleProGlyCyseProProthrmAlaGluAlaLeuLeuTyrGlyIleLeuGln 197  
Db 610 CATCTAGCTCCCTCGGTGGTCCACCACTGCTGAGGCACTAGTACGCTTCTTCACT 669  
Qy 197 uGlnArgLysIleLysArgGluArgArgLeuGlnIleTyrTyrArgArg 213  
Db 670 CCAAAAGAAATCAACAGCGCTAGAGATTCTTCACTGCTGAGCAAG 718

## RESULT 8

US-10-425-114-16284  
; Sequence 16284, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 16284  
; LENGTH: 886  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3062-027-H6\_FLI  
US-10-425-114-16284

## Alignment Scores:

Pred. No.:	2.18e-85	Length:	886
Score:	737.50	Matches:	143
Percent Similarity:	75.70%	Conservative:	19
Best Local Similarity:	66.82%	Mismatches:	44
Query Match:	65.97%	Indels:	8
DB:	17	Gaps:	2

US-09-525-867-1 (1-213) x US-10-425-114-16284 (1-886)

Qy 7 ProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSerSerValaGlyProAlaValaGln 26  
Db 9 CTTGTCACGAGGTGAGAAACCTTAGCCACCAACCATGCGCTTCTCCGCGCACCGC 68  
Qy 27 AlaArgGlyVala-----HisGlnSerValaAlaThrAspGlyProSe 40

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Db      69 GCGGCTGGCCCTCTTCCACCCCGGCGCTACTCCGCTGCGCGGCGCCCTC 128
Qy      40 rSerThrGlnProIleuProlysalAlaValAlaProlyProSerSerArgI 60
Db      129 CCCGACCTCCCCACGG--CCATACCGGGGCGCCCGCCACCGGGGATGTCACAAACGCC 185
Qy      60 yGluTyrValAlaAlaIleuAspAspLeuValaSerThrAlaArgArgSerSerLeuTr 80
Db      186 CGAGTTCGTGCTCTTAAGGTGACGACCTGATGAACTGGGCGCTAAAGGCTCGATCTG 245
Qy      80 pPrometThrPheGlyLeuAlaCysCysAlaValGluMetMetHisMetAlaIaProAr 100
Db      246 GCCCATGACCTTGGGCTGCTGCTGCGCGCGGTGAGATGATGACCGCGGCGGCTCCCG 305
Qy      100 gTyrAspMetAspArgPheGlyValAlaPheArgIaSerProArgIaSerAspValMe 120
Db      306 CTACGACTTCGACCGGCTGCGGCTCATCTCCGTCGCGCGCGGCAAGTCCGATTCAT 365
Qy      120 tIleValAlaGlyThrLeuThrAsnLeuMetAlaProAlaLeuArgIyValaTyrAspG 140
Db      366 GATCGTCCGCGGACGCTACCAACAAAGATGCTCCGCGCTCCGCAAGGTTTATGACCA 425
Qy      140 nMetProGlnProArgIyTyrValAlaSerMetGlySerCysAlaAsnGlyGlyIyTyr 160
Db      426 AATGCTGAGCCTAGGTGGTTATTCAATGGGCACTGTCGCAACGCGTGTGATCTA 485
Qy      160 rHisTyrSerTyrSerValAlaArgGlyCysAspArgIleValaProValAspIleTyr 180
Db      486 CCATTACTCTTACTCTGTGTGACGTGATGACCGATATGTCCTGTGACATCTACGT 545
Qy      180 eProGlyCysProProThrAlaGluAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArg 200
Db      546 CCCGGGGTGGCCACCACTGCTGAGGACGCTGTCAGGGGCTTTCACCTCCAAAGAA 605
Qy      200 sIleLysArgGlnArgArgLeuGlnIleTyrTyrArgArg 213
Db      606 GATCAACAGCGCTAAGGATTTCTTCACTGTCGACCAAG 645

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## RESULT 9

```

US-10-425-114-6711
; Sequence 6711, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 6711
; LENGTH: 949
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700576010_FLI
US-10-425-114-6711

```

## Alignment Scores:

```

Pred. No.: 2,39e-85 Length: 949
Score: 737.50 Matches: 143
Percent Similarity: 75.70% Conservative: 19
Best Local Similarity: 65.82% Mismatches: 44
Query Match: 65.97% Indels: 8
DB: 17 Gaps: 2

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\* US-09-525-867-1 (1-213) x US-10-425-114-6711 (1-949)

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Qy      7 ProGlyLeuArgGlyPheArgIleuGlyLeuArgSerSerValaGlyProAlaValaGln 26
Db      29 CCTCGTCCACGAGGTGAGGAAACCTTACGACCAACCAATGCGTGTCTCCCGGACCGC 88
Qy      27 AlaArgGly-Vala-----HisGlnSerValaIaThrAspGlyProSe 40
Db      89 GCGGCTGGCCCTCTTCCACCCCGGCGCTACTCCGCTGCGCGGCTCTCGGCGCCCTC 148
Qy      40 rSerThrGlnProIleuProlysalAlaValAlaProlyProSerSerArgI 60
Db      149 CCCGACCTCCCCACGG--CCATACGGGGGCGCCCGCCACCGCGCATGTCAGAACAGCGC 205
Qy      60 yGluTyrValAlaAlaIleuAspAspLeuValaSerThrAlaArgArgSerSerLeuTr 80
Db      206 CGAGTTCGTGCTCTTAAGGTGACGACCTGATGAACTGGGCGCTAAAGGCTCGATCTG 265
Qy      80 pPrometThrPheGlyLeuAlaCysCysAlaValGluMetMetHisMetAlaIaProAr 100
Db      266 GCCCATGACCTTGGGCTGCTGCTGCGCGGTGAGATGATGACCGCGGCGGCTCCCG 325
Qy      100 gTyrAspMetAspArgPheGlyValAlaPheArgIaSerProArgIaSerAspValMe 120
Db      326 CTACGACTTCGACCGGCTGCGGCTCATCTCCGTCGCGCGCGGCAAGTCCGATTCAT 385
Qy      120 tIleValAlaGlyThrLeuThrAsnLeuMetAlaProAlaLeuArgIyValaTyrAspG 140
Db      386 GATCGTCCGCGGACGCTACCAACAAAGATGCTCCGCGCTCCGCAAGGTTTATGACCA 445
Qy      140 nMetProGlnProArgIyTyrValAlaSerMetGlySerCysAlaAsnGlyGlyIyTyr 160
Db      446 AATGCTGAGCCTAGGTGGTTATTCAATGGGCACTGTCGCAACGCGTGTGATCTA 505
Qy      160 rHisTyrSerTyrSerValAlaArgGlyCysAspArgIleValaProValAspIleTyr 180
Db      506 CCATTACTCTTACTCTGTGTGACGTGATGACCGATATGTCCTGTGACATCTACGT 565
Qy      180 eProGlyCysProProThrAlaGluAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArg 200
Db      566 CCGTGGGTGGCCACCACTGCTGAGGACGCTGTCAGGGGCTTTCACCTCCAAAGAA 625
Qy      200 sIleLysArgGlnArgArgLeuGlnIleTyrTyrArgArg 213
Db      626 GATCAACAGCGCTAAGGATTTCTTCACTGTCGACCAAG 665

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## RESULT 10

```

US-10-425-115-3877
; Sequence 3877, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 3877
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_103539C.1
US-10-425-115-3877

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## Alignment Scores:

```

Pred. No.: 4.03e-85 Length: 1394
Score: 737.50 Matches: 143
Percent Similarity: 75.70% Conservative: 19
Best Local Similarity: 66.82% Mismatches: 44

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Query Match: 65.97% Indels: 8  
DB: 18 Gaps: 2  
US-09-525-867-1 (1-213) x US-10-425-115-3877 (1-1394)

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QY 7 ProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSerSerValGlyProAlaValAln 26
DB 240 CCTGTCACACGAGGTGAGGAAACCTTAGCCGACCCAGCCATGCGTTGGTCCCGCCACCGC 299
QY 27 AlaArgGlyVal-----HisGlnSerValAlaThrAspGlyProse 40
DB 300 GCGGCTGGCCCTCTTCACCCCGCGGCGTACTCCGCTCCGCTGCTGGCGGCGCTC 359
QY 40 rSerThrGlnProAlaLeuProlyAlaArgAlaValAlaProlyProSerSerArgG 60
DB 360 CCCGACGCCCCACGCG---CCATACGGGGGGGGCCCCCGCCGCGGATGTGAAGACGCG 416
QY 60 yGluTyValValAlaLeuAspAspLeuValAsnTrpAlaArgArgSerSerLeuTr 80
DB 417 CGAGTTGCGGTCTTAAGGTGAGACGACCTGATGAATGGCGGCTAAGGCTCGATCTG 476
QY 80 pPromeThrPheGlyLeuAlaCybCybAlaValAlaGluMetMetHisMetAlaAlaProAr 100
DB 477 GCCCATGACCTTCGCGGCTCGCTGCGCGGTGAGATGATGACACGCGCGCGCTCCG 536
QY 100 gTyAspMetAspArpPheGlyValAlaPheArgAlaSerProArgGlnSerAspValMe 120
DB 537 CTACGACTTCGACCGGCTTCGCGCTCATCTTCCTCCGCGCGCGCGCGCTCGATTGAT 596
QY 120 tLeValAlaGlyThrLeuThrAsnLeuMetAlaProAlaLeuArgLyValTyAspG 140
DB 597 GATCGTCGCGCGGACGCTCACCAACAGATGCTCCGCGCTCCGCGCGCGGCTTATGACCA 656
QY 140 mMerProGluProArgTyValAlaSerMetGlySerCybAlaAsnGlyGlyTyTy 160
DB 657 AATCCCTGAGGCTGAGGTGATTATTCATGAGGACGCTGACCAACGCTGTGATGATCTA 716
QY 160 rHisTySerTySerValAlaArgGlyCybAspArgIleValProValAspIleTyTy 180
DB 717 CCATTACTCTTACTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 776
QY 180 eProGlyCybProProThraAlaGluAlaLeuLeuTyGlyIleLeuGlnLeuGlnArgLy 200
DB 777 CCTGGGAGGCCACCAACTGCTGAGGACCTGCTGACGCGGCTTCTTCAAGTCCAAAGAA 836
QY 200 gIleLeuArgGluArgArgLeuGlnIleTyTyArgArg 213
DB 837 GATCAACAGGCGTAAGATTCTTCACTGCTGAGCAAG 876
```

RESULT 11  
US-10-425-115-3875

```
; Sequence 3875, Application US10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 3875
; LENGTH: 1840
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_103537C.1
US-10-425-115-3875
```

Alignment Scores:

Pred. No.: 1.07e-84 Length: 1840  
Score: 735.50 Matches: 144  
Percent Similarity: 74.65% Conservative: 18  
Best Local Similarity: 66.36% Mismatches: 47  
Query Match: 65.79% Indels: 8  
DB: 18 Gaps: 2

```
US-09-525-867-1 (1-213) x US-10-425-115-3875 (1-1840)
QY 4 LeuSerAlaProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSerSerValGlyPro 23
DB 819 CTTCGCTCTCTCTTCCACGAGGTGAGGAAACCTTAGCCAGTACCATGCGGTTGCTCC 878
QY 24 AlaValAlaArgGly-----Val-HisGlnSerValAlaThrAs 37
DB 879 GCGGACGCGACAGGTGGCTTCTCTCTACCCCGCGGTGATCTCCGCGCGCGCTGCG 938
QY 37 pGlyProSerSerThrGlnProAlaLeuProlyAlaArgAlaValAlaProlyProse 57
DB 939 GGGGCGCTCCCGACCTCCACGCG---CCATACGGGGGGCGCGCCCGCGCGATGTC 995
QY 57 rSerArgGlyGluTyValValAlaLeuAspAspLeuValAsnTrpAlaArgArgse 77
DB 996 GAAGACGCGCGAGTTCGTGCTTCACAGTTGATGACTGATGAACTGGCGCGCTAAGG 1055
QY 77 rSerLeuTrpPromeThrPheGlyLeuAlaCybCybAlaValAlaGluMetMetHisMetAl 97
DB 1056 CTCGATTGGCCCATGACCTTCGCGGCTCGCTGCGCGGCTCGAGATGATGACGCGCG 1115
QY 97 aAlaProArgTyAspMetAspArpPheGlyValAlaPheArgAlaSerProArgGlnse 117
DB 1116 GCGCTCCGCTACGACTTCGACCGGCTCGGCTCATCTTCCTCCGCTCCGCGCGCGCAAGTC 1175
QY 117 rAspValMetIleValAlaGlyThrLeuThrAsnLeuMetAlaProAlaLeuArgLyVal 137
DB 1176 CGATTGATGATGATCTTCGCGCGGACGCTCACCAACAAATGCTTCAAGCTCCGCAAGT 1235
QY 137 tTyAspGlnMerProGluProArgTyValAlaSerMetGlySerCybAlaAsnGlyGly 157
DB 1236 TTATGACCAAAATGCTTACGCTTACCTGATGATGATGATGATGATGATGATGATGATGAT 1295
QY 1296 TGATGATACCATTAATCTTACTCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 1355
QY 157 yGlyTyTyrHisTySerTySerValAlaArgGlyCybAspArgIleValProValAs 177
DB 1296 TGATGATACCATTAATCTTACTCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 1355
QY 177 pIleTyTrIleProGlyCybProProThraAlaGluAlaLeuLeuTyGlyIleLeuGlnIle 197
DB 1356 CATCTACGTCCCTGGGTGCCACCAACTGCTGAGGACCTGCTGATGCGGTGTTCTTCAAGCT 1415
QY 197 uGlnArgLyseIleLeuArgGluArgArgLeuGlnIleTyTyArgArg 213
DB 1416 CCAAAGAAAGATCAACAGGCGTAAGATTCTTCACTGCTGAGCAAG 1464
```

RESULT 12  
US-10-320-797-2049

```
; Sequence 2049, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2049
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Cryptococcus neoformans
```



US-10-320-797-2049

## Alignment Scores:

Pred. No.:	1,05e-84	Length:	753
Score:	731.50	Matches:	140
Percent Similarity:	72.69%	Conservative:	17
Best Local Similarity:	64.81%	Mismatches:	18
Query Match:	65.43%	Indels:	41
DB:	17	Gaps:	2

US-09-525-867-1 (1-213) x US-10-320-797-2049 (1-753)

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QY 39 ProSerSerThrGlnProAlaLeuProlysalarg-----AlaValAla 53
DB 103 CCGGCGCGGTTCAGACCCGCACTGCACTCGCGCTCCGCTCCAGACACCGCGCTGCC 162
QY 54 Prolys----- 55
DB 163 CCGAGGCCCAACACACCACTCGGCATCACTCGTACACCACTCGCCCTCCACACT 222
QY 56 -----Proser 57
DB 223 CTGCCAGACACCACTCGCCCAAGAAAGACACCACTTGAGTCTCGAGACACTAGA 282
QY 58 SerArgGlyGlyValAlaValAlaValLeuAspAspleuValAsnTrpAlaArgSer 77
DB 283 AACGCGCCGAGTATGCTCTTCAACGCTCGACACAGATTGTCACTGCGGCGCAAGGG 342
QY 78 SerLeuTrpProMetThrPheGlyLeuAlaCysCysAlaValGlnMetMetHisMetAla 97
DB 343 TCCATGTGCGCCCAATGACTTGTGTGCTCGCTGCTGCGCGCGGAAATGATGCATGCT 402
QY 98 AlaProArgTrpAspMetAspArgPheGlyValAlaPheArgAlaSerProArgGlnSer 117
DB 403 GCGCGCCGATATGATCAAGATGACCTGCTGCTGCTTCCGAGCGTCCCGCAGACAGGT 462
QY 118 AspValMetLeuValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysVal 137
DB 463 GATGTTATGATTGTACAGACTTCTTAAACAAACAGATGCTGCTGCTGAGAAAGTG 522
QY 138 TyrAspGlnMetProGlnProArgTrpValAlaValSerMetGlySerCysAlaAsnGly 157
DB 523 TACGACCAATGCCGAGACCCGAGTGGCTATTCTTATGAGGTTCATGCGCCAAATGGCGGT 582
QY 158 GlyTrpTrpHisLeuSerTrpSerValValArgGlyCysAspArgLeuAlaProValAsp 177
DB 583 GGTACTACCACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642
QY 178 IleTrpIleProGlyCysProProThrAlaGlnAlaLeuLeuTrpGlyIleLeuGlnLeu 197
DB 643 ATCTATGTCCCGGATGCTCTCCACCGCGCGGCGCTTCTTCAAGGAATGCTCAATTA 702
QY 198 GlnArgLysIleLysArgGlnArgLysLeuGlnIleTrpTrpArgArg 213
DB 703 ATGCAAAAGATGAGGCGGTAAACAGACAGTGTGCGATGCTAACGAGAG 750
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RESULT 13  
US-10-424-599-6216/c; Sequence 6216, Application US/10424599  
; Publication No. US20040031072A1

## GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53223) B  
CURRENT APPLICATION NUMBER: US/10/424, 599  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 6216  
LENGTH: 1356

TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_105622C.1  
US-10-424-599-6216

## Alignment Scores:

Pred. No.:	4.92e-84	Length:	1356
Score:	729.00	Matches:	137
Percent Similarity:	76.53%	Conservative:	26
Best Local Similarity:	64.32%	Mismatches:	50
Query Match:	65.21%	Indels:	0
DB:	17	Gaps:	0

US-09-525-867-1 (1-213) x US-10-424-599-6216 (1-1356)

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QY 1 MetAlaValLeuSerAlaProGlyLeuArgGlyPheArgIleLeuGlyLeuArgSer 20
DB 1236 ATGCTCTTCTGATGATGAGGCTTCTTCACTGCTTCCCTCCAGCTGTTCCCTCAAGAGTT 1177
QY 21 ValGlyProAlaValAlaGlnAlaArgGlyValHisGlnSerValAlaThrAspGlyProSer 40
DB 1176 GTTTCCTCCACACCAAGCTCCCATCTCTTAAGCATCAACATCCACACCGCCGCC 1117
QY 41 SerThrGlnProAlaLeuProlysalargAlaValAlaProlysProSerSerArgGly 60
DB 1116 CCATATGCCCGCCACCGGCTCCGCTCCCTCCCGCGCGGTGCGAGGCGGCG 1057
QY 61 GlnTrpValAlaValAlaLysLeuAspAspleuValAsnTrpAlaArgSerSerLeuTrp 80
DB 1056 GAGTTCGTGATCTCGAAGGTGACATCTGATGAACTGGCCCGCGCGGCTCTCATGCG 997
QY 81 PromerThrPheGlyLeuAlaCysCysAlaValGlnMetMetHisMetAlaAlaProArg 100
DB 996 CCATATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 997
QY 101 TyrAspMetAspArgPheGlyValAlaValPheArgLaseProArgGlnSerAspValMet 120
DB 936 TACGATCTGACCGGCTTGGCATCATTTTACGCGCCGACCCCTGCGCATGTCATG 877
QY 121 IleValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysValTyrAspGln 140
DB 876 ATGCTGCTGCGACCTTCCACCAACAGATGCTCCCTCTTCCGAAAGTTATGACCA 817
QY 141 MetProGlnProArgTrpValAlaValSerMetGlySerCysAlaAsnGlyGlyTrp 160
DB 816 ATGCTGAGCTTATATGAGTGTCTCAATGAGAGATGCTATAGAGAGAGATCTAC 757
QY 161 HisTrpSerTrpSerValAlaArgGlyCysAspArgIleValProValAspIleTrpIle 180
DB 756 CATTACTTCACTCCGATGTTGCGGAGTGTGACAGATTTCTTGTACATATATAT 697
QY 181 ProGlyCysProProThrAlaGlnAlaLeuLeuTrpGlyIleLeuGlnLeuGlnArgLys 200
DB 696 CCAAGCTGTCTTCAACTGCTGAGGCTTGTGCTGATGAGACTCTCCACGTCAGAAAAAG 637
QY 201 IleLysArgGlnLysArgLeuGlnIleTrpTrpArgArg 213
DB 636 ATCAATAGGCGCAAGACTTCTCATATGTTGAGTGAAG 598
```

RESULT 14  
US-10-425-114-36399; Sequence 36399, Application US/10425114  
; Publication No. US20040034888A1

## GENERAL INFORMATION:

APPLICANT: Lin, Jindong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven B.  
APPLICANT: Tabaska, Jack B.  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
Plants and Uses Thereof for Plant Improvement



FILE REFERENCE: 38-21(5313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 36399  
LENGTH: 863  
TYPE: DNA  
ORGANISM: Zea mays subsp. mexicana  
FEATURE:  
OTHER INFORMATION: Clone ID: UC-ZMROTBSINT093D10\_FLI  
US-10-425-114-36399

Alignment Scores:  
Pred. No.: 5.63e-84 Length: 863  
Score: 726.50 Matches: 133  
Percent Similarity: 84.09% Conservative: 15  
Best Local Similarity: 75.57% Mismatches: 27  
Query Match: 64.98% Indels: 1  
DB: 17 Gaps: 1

US-09-525-867-1 (1-213) x US-10-425-114-36399 (1-863)

Qy 38 G l y p r o s e r s e r t h r i n p r o a l a l e u p r o l y s a l a r g l a l a v a l a a p r o l y s e r s e r 57  
D b 4 G G C C C C T C C C G A G C T C C C C A G C G - - C C A T A C G G G G G C C C C C C C A C C G C G A T G C G 60  
Qy 58 S e r a r g l y g l u t y r v a l v a l a l y l e u a p a p l e u a l a n t p r a l a r g s e r 77  
D b 61 A A G A C G C C G A G T T G T G T C T A G G T G A C G A C T G A T A C T G G C G C G T A G G G C 120  
Qy 78 S e r l e u t r p r o m e t t h r p h e g l y l e u a l a c y s c y s a l a v a l a g l u m e t m e t h i s m e c a l a 97  
D b 121 T C G A T T C G C C C A T G A C C T T C G G G C T G C G C G C G G T G A G A T G A T G A C A G C C G C C 180  
Qy 98 A l a p r o a r g t y r a p m e t a s p a r g p h e g l y v a l v a l p h e a r g l a s e r p r o a r g l i n s e r 117  
D b 181 G C G T C C C G C T A C G A C T T C G A C C G G T T C G C G C T C C T C C G C C G C C A G T C C 240  
Qy 118 A s p a l m e t i l e v a l a l a g l y t h r l e u t h r a n l y s m e t a l p r o a l a l e u a r g l y s e r 137  
D b 241 G A T T G C A T G A T C T G C G C G C A C G C T C A C C A A G A T G G C T C C G C C C T C C G A G G T T 300  
Qy 138 T y r a p g l i m e t p r o g l u p r o a r g t y r v a l v a l s e r m e t g l y s e r c y s a l a a n g l y g l y 157  
D b 301 T A T A C C A A A G C C T G A G C C T A G G T A T T T C A A T G G C A G C T G T G C C A A G C G T G C T 360  
Qy 158 G l y t y r t y r i s t y r s e r t y r s e r v a l v a l a r g l y c y s a p a r g l e v a l p r o v a l a s p 177  
D b 361 G G A T A C T A C C A T T A C T C T A C T G T T G T A C G T G A T G A C C G T A T G A T C C T G T G A C 420  
Qy 178 I l e t y r i l e p r o g l y c y s p r o p r o t h r a l a g l u a l e u l e u t y r g l y l l e u g l i n l e u 197  
D b 421 A T C A T A C G C C C T G A G T G C C A C C A A C T G C T A G A C A C G C G T A G C G G T T C T C A G C T C 480  
Qy 198 G l n a r g l y s i l e l y s a r g l u a r g a r g h e u g l i n l e t r p l y r a r g a r g 213  
D b 481 C A A A A A A G A T C A A C A G C C G T A A G G A T T T C C T C A C T G C T G A C C A A G 528

RESULT 15  
US-10-424-599-6217/c  
Sequence 6217, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Zhou Yihua  
APPLICANT: Kovalic David K  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(5323)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 6217  
LENGTH: 1532  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(1532)  
OTHER INFORMATION: unsure at all n locations  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_105623C.1  
US-10-424-599-6217

Alignment Scores:  
Pred. No.: 1.92e-83 Length: 1532  
Score: 725.00 Matches: 136  
Percent Similarity: 76.53% Conservative: 27  
Best Local Similarity: 63.85% Mismatches: 50  
Query Match: 64.85% Indels: 0  
DB: 17 Gaps: 0

US-09-525-867-1 (1-213) x US-10-424-599-6217 (1-1532)

Qy 1 M e c h a l a v a l l e u s e r a l a p r o g l y l e u a r g l y p h e a r g l i l e u g l y l e u a r g s e r 20  
D b 1006 A T G C T C T T C T G A C T C A G C C T C T T C A C G C T T C C C T C A G C G T T C C C T C A A A G G G T A 947  
Qy 21 V a l g l y p r o a l a v a l a g l n a l a r g l y v a l h i a g l i n s e r v a l a l a t h r a p g l y p r o s e r 40  
D b 946 G T T T C A C T C C A C A C A G C C T C C A C T C T T G A A C C A T C C C A T C A C A G C C A G C C T A C A 887  
Qy 41 S e r t h r i n p r o a l a l e u p r o l y s a l a r g l a l a v a l a p r o l y s p r o s e r s e r a r g l y 60  
D b 886 C C A T A T G C C C C G C A C C G C C T C C G C G C T T C C T C C C C G C G G C G T T C A A G G C G C G C 827  
Qy 61 G l u t y r v a l v a l a l y l e u a p a p l e u a l a n t p r a l a r g a r g s e r s e r l e u t r p 80  
D b 826 G A G T T C G A T T C G A A G T G A G A G A T C T G A T G A A C T G G C C C C G C G C C T C A C T G G 767  
Qy 81 P r o m e t t h r p h e g l y l e u a l a c y s c y s a l a v a l a g l u m e t m e t h i s m e c a l a l a p r o a r g 100  
D b 766 C C C A T G A C C T T G G C C T T G C G C G C C C C T C C A A A T G A T G C A C A C C G G C C G C C C G C 707  
Qy 101 T y r a p m e t a s p a r g p h e g l y v a l v a l p h e a r g l a s e r p r o a r g l i n s e r a s p a l m e t 120  
D b 706 T A C A T C T C A C A C C G C T T C G G A T C A T T T T C A G C C C A G C C T G C C A G T C G A T T G A T G 647  
Qy 121 I l e v a l a l a g l y t h r l e u t h r a n l y s m e c a l p r o a l a l e u a r g l y s e r v a l t y r a p g l i n 140  
D b 646 A T C G T C C C G C A C T C T C A C C A A A G A T G G C T C C G C T T C C C A A G G T T A T G A C C A A 587  
Qy 141 M e t p r o g l u p r o a r g t y r v a l v a l s e r m e t g l y s e r c y s a l a a n g l y g l y g l y t y r t y r 160  
D b 586 A T G C T A G C C T A G A T G G T G T C A T A T G G A A G T T G T A T A T G A G A G G A T A C T A C 527  
Qy 161 H i s t y r s e r t y r s e r v a l v a l a r g l y c y s a p a r g l e v a l p r o v a l a s p l e t y r i l e 180  
D b 526 C A T T A C T C T A C C G T A G T T C G G G A T G A C A G A T T G T C C T G T T G A C A T A T A T G T T 467  
Qy 181 P r o g l y c y s p r o p r o t h r a l a g l u a l e u l e u t y r g l y l l e u g l i n l e u g l n a r g l y s 200  
D b 466 C C A G C T G T C C T C C A C T G C T G A G C C T T T G C T A T G A C A C T C C A G C G T C C A G A A A A A G 407  
Qy 201 I l e l y s a r g l u a r g a r g h e u g l i n l e t r p l y r a r g a r g 213  
D b 406 A T C A A T A G G C G C A A A G A C T T C C T C A C T G T G A C A A A G 368

Search completed: March 22, 2005, 07:40:37  
Job time : 582 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 22, 2005, 04:10:57 ; Search time 182 Seconds  
(without alignments)  
1914.983 Million cell updates/sec

Title: US-09-525-867-1  
Perfect score: 1118  
Sequence: 1 MAVISAPGLGFRILGRSS.....ILOQRKIKRRRLQIYYRR 213

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1202784 segs, 81818359 residues  
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool\_h/US09525867/runat\_21032005\_055410\_1201/app.query.fasta\_1.391  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62 -TRANS=human40.cdt  
-LIST=45 -DOCALLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptlo -NOBM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USRR=US09525867.cgn2\_1.1\_69@runat\_21032005\_055410\_1201 -NCPU=6 -ICPU=3  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	100.0	772	4	US-09-620-312D-670
2	756.5	67.7	2378	4	US-09-270-767-14895
3	542	48.5	615	4	US-09-248-786A-2829
4	449	40.2	4403765	3	US-09-103-840A-2
5	449	40.2	4411529	3	US-09-103-840A-1
6	440	39.4	966	4	US-09-253-991A-14622
7	436	39.0	690	4	US-09-489-039A-5374
8	436	39.0	696	4	US-09-253-991A-15142
9	433	38.7	735	4	US-09-543-681A-43
10	431.5	38.6	58909	4	US-09-596-002-30
11	428	38.3	640681	4	US-09-790-988-1
12	427.5	38.2	708	4	US-09-540-236-467

13	418	37.4	684	4	US-09-328-352-581	Sequence 581, App
C 14	411	36.8	789	3	US-09-020-956-32	Sequence 32, Appl
C 15	411	36.8	789	3	US-09-030-607-32	Sequence 32, Appl
C 16	411	36.8	789	3	US-09-439-313-32	Sequence 32, Appl
C 17	411	36.8	789	3	US-09-352-616A-32	Sequence 32, Appl
C 18	411	36.8	789	3	US-09-232-149A-32	Sequence 32, Appl
C 19	411	36.8	789	4	US-09-159-812-32	Sequence 32, Appl
C 20	411	36.8	789	4	US-09-636-215-32	Sequence 32, Appl
C 21	411	36.8	789	4	US-09-685-166A-32	Sequence 32, Appl
C 22	411	36.8	789	4	US-09-115-453-32	Sequence 32, Appl
C 23	411	36.8	789	4	US-09-688-489-32	Sequence 32, Appl
C 24	411	36.8	789	4	US-09-679-426-32	Sequence 32, Appl
C 25	411	36.8	789	4	US-09-759-143-32	Sequence 32, Appl
C 26	411	36.8	789	4	US-09-651-236-32	Sequence 32, Appl
C 27	381	34.1	275	4	US-09-313-294A-6583	Sequence 6583, Ap
C 28	373	33.4	513	4	US-09-902-540-4615	Sequence 4615, Ap
C 29	373	33.4	27490	4	US-09-902-540-1227	Sequence 1227, Ap
C 30	276	24.7	798	4	US-09-489-039A-2763	Sequence 2763, Ap
C 31	265.5	23.7	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 32	265.5	23.7	1664976	4	US-09-692-570-1	Sequence 2334, Ap
C 33	265	23.7	810	4	US-09-543-681A-2334	Sequence 2, Appl
C 34	105.5	9.4	4403765	3	US-09-103-840A-2	Sequence 1, Appl
C 35	105.5	9.4	4411529	3	US-09-103-840A-1	Sequence 1, Appl
C 36	104.5	9.3	6663	4	US-09-335-011-8	Sequence 12, Appl
C 37	104.5	9.3	7223	4	US-09-335-011-8	Sequence 8, Appl
C 38	104	9.3	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 39	104	9.3	1664976	4	US-09-692-570-1	Sequence 1, Appl
C 40	101	9.0	3524	3	US-08-801-344-7	Sequence 7, Appl
C 41	101	9.0	3524	3	US-09-498-599-7	Sequence 9686, Ap
C 42	98.5	8.8	16448	4	US-09-902-540-1098	Sequence 198, Ap
C 43	98.5	8.8	16450	4	US-09-902-540-1098	Sequence 5379, Ap
C 44	97	8.7	2021	4	US-09-949-016-5379	Sequence 3, Appl
C 45	97	8.7	2022	3	US-08-687-691B-3	

#### ALIGNMENTS

RESULT 1  
US-09-620-312D-670  
Sequence 670, Application US/09620312D  
Patent No. 6569662  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyan  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wehrman, Tom  
APPLICANT: Xue, Aidong J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yundong  
APPLICANT: Wang, Dunhui  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinghast  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and  
FILE REFERENCE: 784CIP2B  
CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: PL\_Fl\_genes Version 1.0  
SEQ ID NO 670  
LENGTH: 772  
TYPE: DNA

ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (24)..(665)  
 US-09-620-312D-670

## Alignment Scores:

Pred. No.:	1,076-121	Length:	772
Score:	1118.00	Matches:	213
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-525-867-1 (1-213) x US-09-620-312D-670 (1-772)

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QY 1 MetAlaValLeuSerAlaProGlyLeuArgGlyPheArgGlyIleLeuGlyLeuAlaGlySerSer 20
DB 24 ATGGCGGTGTGTCTGACGCTCTGGCGCTGGCGGCTTCCGAGTCTTGGTCTGCGCTCCAGC 83
QY 21 ValGlyProAlaValAlaGlyValAlaGlyValAlaGlyValAlaGlyValAlaGlyValAlaGly 40
DB 84 CTGGGCGCGCTGTCAGGACGAGGTCTCATCAGCGTGGCCAGCCAGTGGCCAGC 143
QY 41 SerThrGlnProAlaLeuProLysAlaArgAlaValAlaProLysProSerSerArgGly 60
DB 144 AGCACCCAGCTGCTGCGCCAGAGCCAGGCGTGGCTCCAGAACCCAGCCAGCGGCGC 203
QY 61 GluTyrValAlaAlaValLeuAspLeuValAsnTyrAlaArgArgSerLeuTyr 80
DB 204 GAGTATGTGTGCGCAAGCTGATGACCTGTCACCTGGGCGCGCGGCGGCTCTCTGG 263
QY 81 ProMetThrPheGlyLeuAlaCysCysAlaValAlaGluMetMetHisMetAlaAlaProArg 100
DB 264 CCCATGACCTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 323
QY 101 TyrAspMetAspArgPheGlyValAlaPheArgAlaSerProArgGlnSerAspValMet 120
DB 324 TACGACATGACCGCTTGTGGCGTGTCTCCGCGCAGCCGCGCACTCCGACGCTCATG 383
QY 121 IleValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuAlaGlyValTyrAspGln 140
DB 384 ATGTCGCGCGGACACTCACAAGATGAGCCCGAGGCTTCCGAGGCTTCCGAGGCTTCCGAGGCT 443
QY 141 MetProGlnProArgTyrValAlaSerMetGlySerCysAlaAsnGlyGlyTyrTyr 160
DB 444 ATGCGCGAGCCGCGCTACGTGTCTCCATGGGAGCTGCGCCAGAGGAGGCTACTAC 503
QY 161 HisTyrSerTyrSerValAlaArgGlyCysAspArgIleValProValAspIleTyrIle 180
DB 504 CACTATTCTCTACTCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 563
QY 181 ProGlyCysProProThrAlaGlyAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArgGly 200
DB 564 CCAGGCTCCCACTACCGCGCGAGGCGCTGCTTACGGCATCTCTGACGCTGCAGAGAGAG 623
QY 201 IleLysArgGlyAlaArgArgLeuGlnIleTyrTyrArg 213
DB 624 ATCAAGCGGAGCGAGAGCTGCAATCTGTACCGCAGG 662

```

## RESULT 2

US-09-270-767-14895  
 Sequence 14895, Application US/09270767  
 Patent No. 6703491  
 GENERAL INFORMATION:  
 APPLICANT: Homburger et al.  
 TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 FILE REFERENCE: File Reference: 7326-094  
 CURRENT APPLICATION NUMBER: US/09/270,767  
 NUMBER OF SEQ ID NOS: 62517  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 14895

LENGTH: 2378  
 TYPE: DNA  
 ORGANISM: *Drosophila melanogaster*  
 US-09-270-767-14895

## Alignment Scores:

Pred. No.:	1,686-78	Length:	2378
Score:	756.50	Matches:	141
Percent Similarity:	83.76%	Conservative:	24
Best Local Similarity:	71.57%	Mismatches:	26
Query Match:	67.67%	Indels:	6
DB:	4	Gaps:	2

US-09-525-867-1 (1-213) x US-09-270-767-14895 (1-2378)

```

QY 18 ArgSerSerValGlyProAlaValAlaGlyValAlaGlyValAlaGlyValAlaGlyValAlaGly 37
DB 1235 CGCTCTGAATTGGCCCTGGT-----GGCCAAACAAACCCCTTCCAGTTCGCAAGT 1288
QY 38 GlyProSerSerThrGlnProAlaLeuProLysAlaArgAlaValAlaProLysProSe 57
DB 1289 GGCCTAAATCTGCCAAGAGGGCTA-----CTCTCCGTTCCGCAACCAACAGT 1339
QY 57 rSerArgGlyGluTyrValAlaAlaLysLeuAspLeuValAsnTyrAlaArgSe 77
DB 1340 CTCGCTTGGGAGTGTCTACTGGCCAGACTGACGATGCTGCTCACTGGGGTCCGACAGG 1399
QY 77 rSerLeuTyrProMetThrPheGlyLeuAlaCysCysAlaValAlaGluMetMetHisMetAl 97
DB 1400 CTGATCTGGCCCACTGCTTGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1459
QY 97 AlaProArgTyrAspMetAspArgPheGlyValAlaPheArgAlaSerProArgGlnSe 117
DB 1460 TGCTTCGCGCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1519
QY 117 rAspValMetIleValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeuAlaGlyVal 137
DB 1520 CGATGTCAATCATCGTGTGCGTGGACCGCTGACCAAAATGGACCCGCTTGGAAAGGT 1579
QY 137 TyrAspGlnMetProGluProArgTyrValAlaSerMetGlySerCysAlaAsnGly 157
DB 1580 CTACGACCAAAATGGCCCGGACCGTGGTGCATCTCATGAGGAGGCTGCGCAACGCGG 1639
QY 157 yGlyTyrTyrHisTyrSerTyrSerValAlaArgGlyCysAspArgIleValProValAs 177
DB 1640 CGGCTACTACATTAATCTGACTTCCGTTGTCGCGTGGCGGAGGCGCTCATGTACGGGCTTTGCACT 1699
QY 177 PileTyrIleProGlyCysProProThrAlaGlyAlaLeuLeuTyrGlyIleLeuGlnLe 197
DB 1700 CATATACGTACCCCGTGTGTCGCGCAACCGCGGAGGCGCTCATGTACGGGCTTTGCACT 1759
QY 197 uGlnArgLysIleLysArgGlyAlaArgArgLeuGlnIleTyrTyrArg 213
DB 1760 GCAGAAAGAGTTTAAGGAGATGAAGAGCTCCAGATGTGTATGAGAG 1808

```

## RESULT 3

US-09-248-796A-2829  
 Sequence 2829, Application US/09248796A  
 Patent No. 6747137  
 GENERAL INFORMATION:  
 APPLICANT: Keith Weinstock et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
 FILE REFERENCE: 107196.132  
 CURRENT APPLICATION NUMBER: US/09/248,796A  
 PRIOR FILING DATE: 1999-02-12  
 PRIOR APPLICATION NUMBER: US 60/074,725  
 PRIOR FILING DATE: 1998-02-13  
 PRIOR APPLICATION NUMBER: US 60/096,409  
 NUMBER OF SEQ ID NOS: 28208  
 SEQ ID NO 2829  
 LENGTH: 615



OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Alignment Scores:  
Pred. No.: 1,996-37  
Score: 449.00  
Percent Similarity: 60.918  
Best Local Similarity: 41.828  
Query Match: 40.164  
Length: 4411529  
Matches: 92  
Conservative: 42  
Mismatch: 38  
Indels: 48  
Gaps: 6

US-09-525-867-1 (1-213) x US-09-103-840A-1 (1-4411529)

```
QY 4 LeuSerAlaProGlyLeuArgGlyPheArgIle-----Leu 15
DB 3511999 ATTCAATGCTCACGAGTGTGTGCTTACGCTATAGTGTGGCGCGCGGGGCGTACGCTG 3512058
QY 16 GlyLeuArgSerSerValGlyProAlaValGlnAlaArgGlyValHisGlnSerValAla 35
DB 3512059 GGATTGAGGTAGGGGGTGGG----- 3512079
QY 36 ThrAspGlyProSerSerThrGlnProAlaLeuProLysAlaArgAlaValAlaProLys 55
DB 3512080 -----CTGGAGAAACAGCTGCC----- 3512097
QY 56 ProSerSerArgGlyGlyIleValValAlaValAlaLeuAspAspLeuValAsnTrpAlaArg 75
DB 3512098 -----GGCGGATCCTGCTGTCTGACCGGTGAGAGAGGTGGCGGCTATGTGCGC 3512145
QY 76 ArgSerSerLeuTrpProMetThrPheGlyLeuAlaCysCysAlaValGlnMetMetHis 95
DB 3512146 AAAAATCCTCTGTGGCGCGGACATTCGATGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 3512205
QY 96 MetAlaAlaProArgTrpArgPheMetAspArgPheGlyValVal-----PheArgAlaSerPro 114
DB 3512206 ACCGCGGAGACCAAGGTTTGTGATGCTGCGCGCTGTGGATGTGAACGGCTTCTCGCGCCG 3512265
QY 115 ArgGlnSerAspValMetIleValAlaGlyThrLeuThrAsnLysMetAlaProAlaLeu 134
DB 3512266 CGGAGGAGCATCTGTGATGCTGTGGCGCGCGGTACAGCAAGATGCGCGCGCTGCTGCTGCTG 3512325
QY 135 ArgLysValIleTrpAspGlnMetProGlnProArgTrpValValSerMetGlySerCysAla 154
DB 3512326 CGGACATCTATGACCAAGATGCGGAGCGCAATGGGTTCTGCGCATGCGGTGTGCGCC 3512385
QY 155 AsnGlyGlyGlyTrpTrpHisTrpSerTrpSerValValaArgGlyCysAspArgGlyIleVal 174
DB 3512386 TCGTCAAGTGGGATGTCAAC---AATATGCGATCGTGCAGCGCGCTGATCATGTGTT 3512442
QY 175 ProValAspIleTrpIleProGlyCysProProThrAlaGlnAlaLeuLeuTrpGlyIle 194
DB 3512443 CCGGTGACATCTTACCTACCGGCTGCGCGCGCGCGCGGAGATGCTGTGACGCAATC 3512502
QY 195 LeuGlnLeuGlnaArgLysIleLys-----ArgGluAspArgLeu 207
DB 3512503 CTGAAGCTGCAGAAAGATTACGACAGATGCGCATTAGTATCAACCGGAGCAACGCTATC 3512562

RESULT 6
US-09-252-991A-14622/c
; Sequence 14622 Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196, 136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074, 788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094, 190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
```

SEQ ID NO 14622  
LENGTH: 966  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14622

Alignment Scores:  
Pred. No.: 6,356-42  
Score: 440.00  
Percent Similarity: 59.03%  
Best Local Similarity: 43.17%  
Query Match: 39.36%  
Length: 966  
Matches: 98  
Conservative: 36  
Mismatch: 61  
Indels: 32  
Gaps: 7

US-09-525-867-1 (1-213) x US-09-252-991A-14622 (1-966)

```
QY 12 PheArgIleLeuGlyLeuArgSerSerValGlyProAlaValGlnAlaArgGlyValHis 31
DB 951 TGGCGGCTTTG-----TCTATCTTGGCGGATCGTGCCTGATGGGCTCGCG 901
QY 32 GlnSerValAlaThrAspGlyProSerSerThrGlnProAlaLeu----- 46
DB 900 AAAGCCGTCCCAAGCGCGAGCGCAAGCTTAAACAAATGAGCTTTGGCGATGCATATCAAA 841
QY 47 -----ProLysAla-----ArgAlaVal 52
DB 840 CTTACCGGATCGATCCGATCGCGCAACGCAATACCGATGAGCGGAACGGGAACC 781
QY 53 AlaProLysProSerSerArgGlyGlu-----TrpValValAlaLysLeuAsp 68
DB 780 GTACCGCACCGGTGTGAGGCGCAGGATTCACAAAGATCTTCATGCGCAACCTGAG 721
QY 69 AspLeu-----ValAsnTrpAlaArgArgSerSerLeuTrpProMetThrPhe 84
DB 720 GATGTGCTGAATCCACCGGTCAACGTGCGGTGCGCAAGATCTGCTGCGCTGCTGCTGCTGCTG 661
QY 85 GlyLeuAlaCysCysAlaValaGlnMetMetHisMetAlaAlaProArgTrpAspMetAsp 104
DB 660 GGGCTGTGCTGTGTGATGAGATGACCAACCGCTTACCGCGCGCGCAAGATATCGCC 601
QY 105 ArgPheGlyVal-----ValPheArgAlaSerProArgGlnSerAspValMetIleValAla 123
DB 600 CCGTTCGCGCGCGCAAGATATCGCGCGCTGCGCGCGCGCGCGCGCATTCATGCTATCGCC 541
QY 124 GlyThrLeuThrAsnLysMetAlaProAlaLeuArgLysValIleTrpAspGlnMetProGln 143
DB 540 GGCACCTGCTTCATCAAGATGCGCGCGCGCTGATCAAGGCGCTTACAGCAAGATGCTCGAA 481
QY 144 ProArgTrpValValSerMetGlySerCysAlaAsnGlyGlyIleTrpTrpHisTrpSer 163
DB 480 CCAAGTGGGTATCTTCATGAGGCTGCTGCGCAATTCGGGGCGCATGTACACATC--- 424
QY 164 TrpSerValValaArgGlyCysAspArgIleValaProValAspIleTrpIleProGlyCys 183
DB 423 TATTCGATGTTCCAGGGGTCACAGATGTTCTCCCGTGAAGTGTATCCCGCGCTGC 364
QY 184 ProProThrAlaGlnAlaLeuLeuTrpGlyIleLeuGlnLeuGlnaArgLysIleArg 203
DB 363 CCGCGCGCGCGAGGCGTTCCTGCAAGGCTTGAATGCTTTCAGGAATTCATCGGCGAG 304
QY 204 GluArgArgLeuGlnIleTrp 210
DB 303 GAGCGCGCGCGCTGCTGCTG 283

RESULT 7
US-09-489-039A-5374
; Sequence 5374 Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709, 2004001
```

;; CURRENT APPLICATION NUMBER: US/09/489,039A  
;; CURRENT FILING DATE: 2000-01-27  
;; PRIOR APPLICATION NUMBER: US 60/117,747  
;; PRIOR FILING DATE: 1999-01-29  
;; NUMBER OF SEQ ID NOS: 14342  
;; SEQ ID NO 5374  
;; LENGTH: 690  
;; TYPE: DNA  
;; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-5374

Alignment Scores:  
Pred. No.: 1.12e-41 Length: 690  
Score: 436.00 Matches: 79  
Percent Similarity: 73.10% Conservative: 27  
Best Local Similarity: 54.48% Mismatches: 37  
Query Match: 39.00% Indels: 2  
DB: Gaps: 2

US-09-525-867-1 (1-213) x US-09-489-039A-5374 (1-690)

QY 67 LeuaphleuValaentTTPAlaArgSerSerLeuTPPrometThPhaglyLeu 86  
DB 151 CTGCATGACATGTAACCTGGGCGCTAAGAACTCAATTGGCCGTACACTTCGCCCTT 210  
QY 87 AlaCyseCybaValaGluMetMetHleMetAlaAlaProArgTYraPmetAspArgPhe 106  
DB 211 TCTTCTCTTATGTGGAATGTGACATTCATCTACCTGGCGTGCATGACGTTGCCGTTT 270  
QY 107 GlyVal---ValPheArgAlaSerProArgInSerAspValMetIleValAlaGlyThr 125  
DB 271 GGGGCAAGAGTTCTGGCGGCTCTCCGCTCAGCGACCTGATGTGTCGGGGAACC 330  
QY 126 LeuThrAsnlyMetAlaProAlaLeuArglyValTYraPglImetProGluProArg 145  
DB 331 TGCCTTACCAAAATGGCGCCGGTATTCAGCGTCTACGATCAGATGCTGAGCCGAAAG 390  
QY 146 TYraValaSerMetGlySerCybaAlaAsnGlyGlyTYrTYrHleTYrSerTYrSer 165  
DB 391 TGGGTATCTTCAATGGGCGCTGGCCCACTCAGCGGAGATGACATC---TATTCC 447  
QY 166 ValValaArgGlyCybaAspArgIleValProValAspIleTYrIleProGlyCybaPro 185  
DB 448 GTCTCCAGGGCGTGAATTAATTCATTCGATGATGATCATCCCGGCTGCCCGCG 507  
QY 186 ThrAlaGluAlaLeuLeuTYrGlyIleLeuGlnLeuGlnArglyIleValArgGlyArg 205  
DB 508 CGTCCGAGGCGCTATATGACAGCGCTGCTGCTGACAGAGTCCATTGTAAAGACGT 567  
QY 206 ArgLeuGlnIleTyr 210  
DB 568 CGTCCGCTCTCATGG 582

RESULT 8  
US-09-252-991A-15142  
; Sequence 15142, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 15142  
; LENGTH: 696  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-15142

Alignment Scores:  
Pred. No.: 1.14e-41 Length: 696  
Score: 436.00 Matches: 86  
Percent Similarity: 69.88% Conservative: 30  
Best Local Similarity: 51.81% Mismatches: 39  
Query Match: 39.00% Indels: 11  
DB: Gaps: 4

US-09-525-867-1 (1-213) x US-09-252-991A-15142 (1-696)

QY 55 LysProSerSerArgly-----GluTYrVal-ValAlaLysLeuAspAspLe 70  
DB 96 CGACCCCGTGGTCCAGGAGGCCAGTTCAAGAACATCTTATGGCAAGCTCGAGGATGT 155  
QY 70 u-----ValSerTPAlaArgAspSerLeuTPPrometThrPheGlyLe 86  
DB 156 GCTGAATCCACCCCTCACTGGGGTGCAGAACTCGCTGCGCTTAACTTCGGGCT 215  
QY 86 uAlaCyseCybaValaGluMetMetHleMetAlaAlaProArgTYraPmetAspArgPhe 106  
DB 216 GTCTGCTCTACGTGAGATGACACCGCTTACCGCGCCGACGATATCGCCGCTT 275  
QY 106 eGlyVal---ValPheArgAlaSerProArgInSerAspValMetIleValAlaGlyThr 125  
DB 276 CGGCGCGAAGTATCCGGGGGTGCGCGCGCAGCGACCTTCAATGTCATGCGCGCAC 335  
QY 125 rLeuThrAsnlyMetAlaProAlaLeuArglyValTYrAspGlnmetProGluProAr 145  
DB 336 CTGCTTCATCAAGATGCGCCCGCTATCCACCGCTTACAGAGATGTCGAACCGAA 395  
QY 145 gTYrValaSerMetGlySerCybaAlaAsnGlyGlyTYrTYrHleTYrSerTYrSe 165  
DB 396 GTGGTATCTTCAATGGGCTGTGCGCAATTCGGCGGAGATGACATC---TATTCC 452  
QY 165 rValaValaArgGlyCybaAspArgIleValProValAspIleTYrIleProGlyCybaPro 185  
DB 453 GTGTGTCCAGGGGTGCAAGATTCCTCCCGGTGGAAGTCAATCCCGGCTGCCCGC 512  
QY 185 oThrAlaGluAlaLeuLeuTYrGlyIleLeuGlnLeuGlnArglyIleValArgGlyArg 205  
DB 513 CGTCCGAGGCGTCTCTGCAAGGCTGATGCTGTGAGAAATTCATCGGACGAGACG 572  
QY 205 ArgLeuGlnIleTyr 210  
DB 573 CGGCGCGCTGTCTGG 588

RESULT 9  
US-09-543-681A-43  
; Sequence 43, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 43  
; LENGTH: 735  
; TYPE: DNA  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-43  
Alignment Scores:  
Pred. No.: 2.78e-41 Length: 735  
Score: 433.00 Matches: 80  
Percent Similarity: 72.41% Conservative: 25  
Best Local Similarity: 55.17% Mismatches: 38



Query Match: 38.73% Indels: 2  
DB: 4 Gaps: 2

US-09-525-867-1 (1-213) x US-09-543-681A-43 (1-735)

```
QY 67 LeuAspAspLeuValAsnTrpAlaArgArgSerLeuTrpProMetThrPheGlyLeu 86
DB 196 TTAACATGACGTTGTGAACCTGGGAGAAAAAATCTTTATATGCCCATAATATTGGTCTT
QY 87 AlaCyCyAlaValAlaGlnMetMetHisMetAlaAlaProArgTyrAspMetAspArgPhe
DB 256 TCCCTGTTGTTACGTTGAATAGTGTACGCTATTACTGCGTCCATGACGTAAGCGGCTTTT
QY 107 Gly---ValValPheArgAlaSerProArgInserAspValMetIleValAlaGlyThr 125
DB 316 GATTCTGAAGATTAAACGCTTCCCTCGTCAAGCTGACTTATAGCGTGTTCAGAGAAC
QY 126 LeuThrAsnLeuMetAlaProAlaLeuArgLysValTyrAspGlnMetProGluProArg 145
DB 376 TGCTTTACAAAGATGCGCCCGCTTAATTCAGGTTTATACATCAGATGTTAGAGCCTAAG
QY 146 TyrValValSerMetGlySerCyAlaAsnGlyGlyTyrTyrHisTyrSerTyrSer 165
DB 436 TGGGTTATTTCCATGAGGAGGCTTGGCTTAACCTGCTGCTATGATGACATC---TATTCG
QY 166 ValValArgGlyCysAspArgIleValProValAspIleTyrIleProGlyCysProPro 185
DB 493 GTACTGCAAGGTGTGATTAATTCATTCCTGATGATGTGATATCCAGAGATGCCACCT
QY 186 ThrValGlnAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArgLysIleLysArgGluArg 205
DB 553 CGTCCAAAGCTTATATGCAAGCATGTGATGTTATTCAGAGATCCATTGTTAAAGACGT
QY 206 ArgLeuGlnIleTyr 210
DB 613 CGCCCATTAATCTTGG 627
```

## RESULT 10

US-09-596-002-30  
Sequence 30, Application US/09596002  
Patent No. 6632636  
GENERAL INFORMATION:  
APPLICANT: Lagace, Robert, E.  
APPLICANT: Patterson, Chandra  
APPLICANT: Berg, Kim, L.  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
FILE REFERENCE: PM-0008-4 US  
CURRENT APPLICATION NUMBER: US/09/596,002  
PRIOR FILING DATE: 2000-06-16  
PRIOR APPLICATION NUMBER: 60/140,121  
PRIOR FILING DATE: 1999-06-18  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PERL Program  
SEQ ID NO 30  
LENGTH: 58909  
TYPE: DNA  
ORGANISM: M. catarrhalis  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte template ID NO. 6632636 30  
PUBLICATION INFORMATION:  
US-09-596-002-30

## Alignment Scores:

Pred. No.: 3 24e-38 Length: 58909  
Score: 431.50 Matches: 88  
Percent Similarity: 67.05% Conservative: 30  
Best Local Similarity: 50.05% Mismatches: 52  
Query Match: 38.60% Indels: 7  
Gaps: 3

US-09-525-867-1 (1-213) x US-09-596-002-30 (1-58909)

```
QY 36 ThrAspGlyProSerSerThrGlnProAlaLeuProLysAlaArgAlaValAlaProLys 55
DB 26810 ACCAACATACCAAGCAATACCCACAAACAAACCGGTGAATCATTTAGCATATCCACAG
QY 56 ProSerSerArgGlyGlyTyrValValAlaLysLeuAspSer-----LeuVal 71
DB 26870 CCGAGGTG-GATTAATAAGTTTTTTTGGCGAGATTGTCGATTGACGCAACACTTGGC
QY 72 AsnTrpAlaArgArgSerSerLeuTrpProMetThrPheGlyLeuAlaCyCyAlaVal 91
DB 26929 AACTGGGGTCCCAAAATCTCTTATGCGCCCTTAAACTTTGGCACAAGCTGTTTATGTC
QY 92 GlnMetMetHisMetAlaAlaProArgTyrAspMetAspArgPheGlyVal---ValPhe 110
DB 26989 GAGTATGACGACGACCTTGACAGGCGTGCATGATTTGCTGCTGTTTGGCGAGAGCTCAT
QY 111 ArgAlaSerProArgGlnInserAspValMetIleValAlaGlyThrLeuThrAsnLysMet 130
DB 27049 CGTCCCTCCCTCCGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG
QY 131 AlaProAlaLeuArgLysValTyrAspGlnMetProGluProArgTyrValValSerMet 150
DB 27109 GCGCTGTGATTTCTCAGGCTGATGACAAATGTTAAGAACTTAATGGGTCAATCTTCATG
QY 151 GlySerCyAlaAsnGlyGlyTyrTyrHisTyrSerTyrSerValValArgGlyCys 170
DB 27169 GGGGCGGTGCCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 171 AspArgIleValProValAspIleTyrIleProGlyCysProProThrAlaGlnAlaLeu 190
DB 27226 GATTAATCTTGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG
QY 191 LeuTyrGlyIleLeuGlnLeuGlnArgLysIleLysArgGluArg 206
DB 27286 ATTCAAGCATCATGCTATTAACAAGAGACATTCAAAAGAACCCCGT 27333
```

## RESULT 11

US-09-790-988-1  
Sequence 1, Application US/0790988  
Patent No. 6632935  
GENERAL INFORMATION:  
APPLICANT: SHIGEMOBU, SHUJI  
APPLICANT: WATANABE, HIDEMI  
APPLICANT: HATTORI, MASAHIRA  
APPLICANT: SAKAKI, YOSHIYUKI  
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS  
FILE REFERENCE: 081356/0159  
CURRENT APPLICATION NUMBER: US/09/790,988  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: JP2000-107160  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 640681  
TYPE: DNA  
ORGANISM: Buchnera sp.  
US-09-790-988-1

## Alignment Scores:

Pred. No.: 3 12e-36 Length: 640681  
Score: 428.00 Matches: 81  
Percent Similarity: 72.41% Conservative: 24  
Best Local Similarity: 55.86% Mismatches: 38  
Query Match: 38.28% Indels: 2  
Gaps: 2

US-09-525-867-1 (1-213) x US-09-790-988-1 (1-640681)

```
QY 67 LeuAspAspLeuValAsnTrpAlaArgArgSerLeuTrpProMetThrPheGlyLeu 86
DB 165027 TTAACATTAATTAATTAATTTGGGTCGAAAAAATCTTTATAGCTTAAATTTGGTCTG 165086
```

```

Qy      87 AlaCysCysAlaValGluMetMetHisMetAlaIaProArgTyrAspMetAspArgPhe 106
Db      165087 TCTTGTGTATGTAAGGAATGTAATGCTTTACTTCCGTTCAATGATGATGCAAGCTTTT 165146
Qy      107 Gly--ValValPheArgAlaSerProArgGlnSerAspValMetIleValAlaGlyThr 125
Db      165147 GGACTGTGAAGTATTAACGTGCTCTCCCTAGACAGCTGATGTCATGTCATGTCAGAGTACG 165206
Qy      126 LeuThrAsnIleMetAlaProAlaLeuArgLysValTyrAspGlnMetProGlnProArg 145
Db      165207 CCATTATTAATAAATGGCCCTCTTATTAAGAGATTATTCAGATCAATATTGAAACCAAA 165266
Qy      146 TyrValValSerMetGlySerCysAlaAsnGlyGlyTyrTyrHisTyrSerTyrSer 165
Db      165267 TGGGTATATTCTATGGGAGCATGTGCGCAATTCTGGCGGAATGATGATATC--TATTCT 165323
Qy      166 ValValArgGlyCysAspArgIleValProValAspIleTyrIleProGlyCysProPro 185
Db      165324 GTTGTTCAGAGATGATAAATTTTGGCGGTGATATTTATATTCCTGTTGTCACCT 165383
Qy      186 ThrAlaGluAlaLeuLeuTyrGlyIleLeuGlnLeuGlnArgLysIleLysArgGluArg 205
Db      165384 CGTCTGTGAAGCATATGCAAGCTTTAATCTGTTGCAAAATTTGATCAATGAAGAAGA 165443
Qy      206 ArgLeuGlnIleTyrP 210
Db      165444 AGGCCGTTATCTCTG 165458

RESULT 12
US-09-540-236-467
; Sequence 467, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540.236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 467
; LENGTH: 708
; TYPE: DNA
; ORGANISM: M.catarhalis
US-09-540-236-467

Alignment Scores:
Pred. No.: 1,16e-40 Length: 708
Score: 427.50 Matches: 87
Percent Similarity: 66.48% Conservative: 30
Best Local Similarity: 49.43% Mismatches: 53
Query Match: 38.24% Indels: 7
DB: 4 Gaps: 3

US-09-525-867-1 (1-213) x US-09-540-236-467 (1-708)
Qy      36 ThrAspGlyProSerSerThrGlnProAlaLeuProLysAlaArgAlaValAlaProLys 55
Db      62 ACCAACATACCAAGCAATACCCACCAACAAGCCGTGAATATCATGATCATCAACCCAAAG 121
Qy      56 ProSerSerArgGlyGlyTyrValValAlaLysLeuAspAsp-----LeuVal 71
Db      122 CCGAGGTC-GATTAATAATGTTTTTTTGGGAGATTGTCCGATTTGACCAACCACTTCC 180
Qy      72 AsnTTPAlaAlaArgArgSerSerLeuTyrProMetThrPheGlyLeuAlaCysCysAlaVal 91
Db      181 AACTGGGGTCCCAAAATCTCTTATGCGCTTAACTTGGACACAGCTGTTGTTATGTG 240
Qy      92 GluMetMetHisMetAlaIaIaProArgTyrAspMetAspArgPheGlyVal---ValPhe 110
Db      241 GAGTATGCCACGACCTTGACAGCGCTGCATATTTGCTCGTTTGGGCGGAGGTCAATT 300
Qy      111 ArgAlaSerProArgGlnSerAspValMetIleValAlaGlyThrLeuThrAsnIleMet 130

```

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Db      301 CGTCCCTCCCTCCCAAGCTGATGTGATGATGGGGGAGAGCTGTTTGTCAAAATG 360
Qy      131 AlaProAlaLeuArgLysValTyrAspGlnMetProGlnProArgTyrValValSerMet 150
Db      361 GCACCTGATGTTCTCAGAGCTGTATGAAACAAATGCTAGAACCCAAAGGTGATCTCCATG 420
Qy      151 GlySerCysAlaAsnGlyGlyTyrTyrHisTyrSerTyrSerValValArgGlyCys 170
Db      421 GGGGCGTGTGCCAATCTCTGGGCGATGTATACATT--TATTGCTGTGTGACGGGGT 477
Qy      171 AspArgIleValProValAspIleTyrIleProGlyCysProProThrAlaGluAlaLeu 190
Db      478 GATAAATCTTGCTGCGATGTATGTTCCGGGGTGTCCGACACGCCGAGGCTTTG 537
Qy      191 LeuTyrGlyIleLeuGlnLeuGlnArgLysIleLysArgGluArgArg 206
Db      538 ATTGAGCATTAATGCTCTTCAAAACTCAATCCAAAGAGAACGCCGT 585

RESULT 13
US-09-328-352-581
; Sequence 581, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC9-03PA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 581
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-581

Alignment Scores:
Pred. No.: 1,44e-39 Length: 684
Score: 418.00 Matches: 78
Percent Similarity: 72.97% Conservative: 30
Best Local Similarity: 52.70% Mismatches: 34
Query Match: 37.39% Indels: 6
DB: 4 Gaps: 3

US-09-525-867-1 (1-213) x US-09-328-352-581 (1-684)
Qy      64 ValAlaLysLeuAspAspLeu-----ValAsnTTPAlaArgArgSerSerLeu 79
Db      115 ATGACTCGTTTAGAGGATGTCTTCATACAGACGTAACAGTGGGACGTAAACCTCTTG 174
Qy      80 TTPProMetThrPheGlyLeuAlaCysCysAlaValGluMetMetHisMetAlaIaPro 99
Db      175 TGGCCATTTAACCTTGGTATCATGTTGTTAGCTTGTAATATGCAACGACCTTAACAGGC 234
Qy      100 ArgTyrAspMetAspArgPheGlyVal---ValPheArgAlaSerProArgGlnSerAsp 118
Db      235 GTGCATGACTGTCTCCGTTTGGTGCAGAGTTATTGTGCTTCACTCGTCAGAGCTAC 294
Qy      119 ValMetIleValAlaGlyThrLeuThrAsnIleMetAlaProAlaLeuArgLysValTyr 138
Db      295 TTGATGATTTGTGACGAGTACTGCTTTGTAATAATGCTCGGTATATCAACGTTTGTAT 354
Qy      139 AspGlnMetProGlnProArgTyrValValSerMetGlySerCysAlaAsnGlyGly 158
Db      355 GAACAAATGTTAGAACCTTAATGAGTATTTCAATGGGTGCTTTCGCAAACTCTGGAGGT 414
Qy      159 TyrTyrHisTyrSerTyrSerValValArgGlyCysAspArgIleValProValAspIle 178
Db      415 ATGTACGACATC--TATTGATGTACAGGTGTACAAATTTATTCCTGTGACGTG 471
Qy      179 TyrIleProGlyCysProProThrAlaGluAlaLeuLeuTyrGlyIleLeuGlnLeu 198

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Db 472 TAGTCCAGGTTGCTCGCTCTGTAAGCATTAATCAAGCATTAAGCTTTTACAA 531  
Qy 199 ArglysllelyeArglyuArg 206  
Db 532 GACCAATTCAATTAGAGCGACGC 555  
RESULT 14  
US-09-020-956-32/c  
Sequence 32, Application US/09020956  
Patent No. 6261562  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiaqun  
APPLICANT: Dillon, David C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
NUMBER OF SEQUENCES: 178  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/020,956  
FILING DATE: 09-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.427C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 622-4900  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-020-956-32  
Alignment Scores:  
Pred. No.: 1,196-38  
Score: 411.00  
Percent Similarity: 62.11%  
Best Local Similarity: 60.00%  
Query Match: 36.76%  
Matches: 114  
Conservative: 4  
Mismatches: 54  
Indels: 21  
Gaps: 2  
US-09-525-867-1 (1-213) x US-09-020-956-32 (1-789)  
Qy 36 ThrspgllyProserSerThnglnProalaLeuProlysaAlaAlaAlaProlys 55  
Db 696 ACCGGGGGCCCGAAGGGGGGAGNCCCTTGGCCNCCAAAGNNAAGGCGGCTTCCCAAA 637  
Qy 56 ProserSerArglygluTyrrValaAlaAlaLeuAspAspLeuValaAsnTrpAlaAr 75  
Db 636 CCCAGNNAAGGGGGGAGGATTTGGGGGCCCAAGGGGATGACTTGTGTG----- 588  
Qy 75 gaTgSerSerLeuTrpPro-----MetThPhaglyLeuAl 87  
Db 587 -----AAACTGGGNCCTCCCGAGNTTTTGGNGGCCNCAAGAACTTTGGGTGNC 535  
Qy 87 aCysCysAlaValaGluMetMetMetMetAlaAla-ProArgTyrrAspMetAspArgphe- 106  
Db 534 CTGNTGNGCCCGGGAGGTGATGNNATNGCAGCAACCCGNNAAAGCAATGNCCTGTTT 475

Qy 107 -GlyValValaPheArgAlaSerProArglnSerAspValMetlleValaAlaGlyThrle 126  
Db 474 GGGGNGNTTTTGGGGCCAGCCGAGCTCTGA-GTNAATGATTTGGGNGGNNANANT 416  
Qy 126 uThrasnlysmetAlaProAlaLeuArglyValTyrrAspGlnMetProGluProArgTy 146  
Db 415 AACCAAAAAGAGGGCCAGGTTTGC-AGGTTTAAGACCAATGCCAGGCCGAGANA 357  
Qy 146 rValaIsereMetGlyserCysAlaenglyGlyTyrrTyrrHisTyrrSerTyrrSerVa 166  
Db 356 AGTGTTTCCANGGGAGTGN-GCCAACGAGNGGGGTAAACCACTATTCTTAATNGT 298  
Qy 166 lValArglyCysAspArglyleValProValaAspIleTyrrlleProGlyCysProthm 186  
Db 297 GGTAGGGGNTGCCAGCGCATTTGGCCCGGAAATTAATCCAGGGTGGCCACCNAN 238  
Qy 186 rAlaGluAlaLeuLeuTyrrlylleuGlnleuGlnArglysllelyeArglyuArg 206  
Db 237 GCGGAGGCCCTGTTTANGGCATCTCGAGCTGACAGAGGAANATCAAGCGGAGCGAG 178  
Qy 206 gLeuGlnlleTyrrArg 213  
Db 177 GCTGCANATTTGGTACCGCAGG 156  
RESULT 15  
US-09-030-607-32/c  
Sequence 32, Application US/09030607  
Patent No. 6262245  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiaqun  
APPLICANT: Dillon, David C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
NUMBER OF SEQUENCES: 224  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,607  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.427C3  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 622-4900  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-030-607-32  
Alignment Scores:  
Pred. No.: 1,196-38  
Score: 411.00  
Percent Similarity: 62.11%  
Best Local Similarity: 60.00%  
Query Match: 36.76%  
Matches: 114  
Conservative: 4  
Mismatches: 54  
Indels: 21  
Gaps: 2

US-09-525-867-1 (1-213) x US-09-030-607-32 (1-789)

```
Oy 36 ThrAapGIProSerSerThrGlnProAlaLeuProLySAIaArgAlaValAlaProLyS 55
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 696 ACCGGGGGCCCCGAAGGGGAGNCANCTGCCNCCAAAGNNAAGAGCGCTGGGTTCCCAA 637
Oy 56 ProSerSerAArgGIyGIuTyrValValAlaLySLeuAapAap-LeuValAenTrpAlaAr 75
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 636 CCCAGNNAANCAGGGGAGGATTTGGGGGCCCAAGGGGATGACTTGTGTG----- 588
Oy 75 gArSerSerLeuTrpPro-----MetThrPheGIyLeuAl 87
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 587 -----AACTGGGNCCTCCCGGAGNTTTTGTGGGCCCNCAAGAACCTTTGGGTTGNC 535
Oy 87 aCySaIaValaGIuMetMetHisMetAlaAla-ProArgTyraPheMetAapArgPhe- 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 534 CTGNTGNCCCGGGAGGTGATGNANATNGCAGCAACCCGNNNAAGACATGGNCCGGTTT 475
Oy 107 -GIyValaPheArgAlaSerProArgGlnSerAapValMetIleValAlaGIyThrLe 126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 474 GGGGNGNTTTTGGGGCCAGCCGNCAGTCTGA-GTNATGATTGTGGCNGNANANT 416
Oy 126 uThrAsnLyMetAlaProAlaLeuArgLyValTyraPheGlnMetProGIuProArgTy 146
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 415 AACCAAAAAGAGGGCCCGAGNGTTTGC-AAAGTTTAAGACCAAGATCCGAGCCCGGANA 357
Oy 146 rValIaSerMetGIySerCySAIaAsnGIyGIuTyrTyraHisTyraSerTyraSerVa 166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 356 AGTGGTTTCCANGGGGAGTGN-gCCAACGNGNGGTAAANACCACTATTCCTAATNGT 298
Oy 166 lValArgGIyCySAaPArgIleValProValAapIleTyriIleProGIyCy8ProProTh 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 297 GGTGAGGGGNTGCCGACGATTTGTGCCGTGAATTAATCCACAGGTGCCACCNAN 238
Oy 186 rAlaGIuAlaLeuLeuTyrgIyIleLeuGlnLeuGlnArgLySileTyraArgGIuArgAr 206
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 237 GGCCGAGGCCCTGTTTANGGCATCTGTGACGTGCAGAGANATCAAGCGGAGCGGAG 178
Oy 206 gLeuGlnIleTrpTyraArg 213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 177 GCTGCANATTGGTACCGCAGG 156
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Search completed: March 22, 2005, 07:50:56  
Job time : 5030 secs

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Db 668 CCGCCGCGCGCGCGCGCGAGACTGTGCGCGCTGTGCTCCGAGCCTGTGTTGTGCTCCGTG 727  
Qy 783 AGGTTGTCAATAAACCTTCCCTCGGGCAAAAAAAAAAAAAA 824  
Db 728 AGGTTGTCAATAAACCTTCCCTCGGGCTGGCGCCCAAAAAA 769

## RESULT 3

US-10-104-047-625  
; Sequence 625, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 625  
; LENGTH: 2818  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-047-625

Query Match 69.1%; Score 569.2; DB 17; Length 2818;  
Best Local Similarity 97.8%; Pred. No. 1.4e-148;  
Matches 577; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 56 GTTGTCTGAAGCCGCGCGCGCAAGATGGGGTGTCTGTCACTCTGCGCCTGCGCGCTTCC 115  
Db 1 GTTGTCTGAAGCCGCGCGCGCAAGATGGGGTGTCTGTCACTCTGCGCCTGCGCGCTTCC 60  
Qy 116 GGATCTCTTGTCTGTGCGCTCCAGCGTGGCCCGGCTGTGTCAGAGCAAGATGTCTCATA 175  
Db 61 GGATCTCTTGTCTGTGCGCTCCAGCGTGGCCCGGCTGTGTCAGAGCAAGATGTCTCATA 120  
Qy 176 GCGTGGCCACCGATGGGCCCAAGACAGACCCAGCCTGCGCTTGCAGAGCCAGAGCCGTGG 235  
Db 121 GCGTGGCCACCGATGGGCCCAAGACAGACCCAGCCTGCGCTTGCAGAGCCAGAGCCGTGG 180  
Qy 236 CTCGCCAACCCAGACCGCGCGCGCGATGTGTGTGGCCCAAGTGTGATCACTCTGCAACT 295  
Db 181 CTCGCCAACCCAGACCGCGCGCGCGATGTGTGTGGCCCAAGTGTGATCACTCTGCAACT 240  
Qy 296 GGGCCCGCGGAGTTCTCTGTGGCCCATGACCTTGGCGCTGGCTGTGCGCCGTGAGAGA 355  
Db 241 GGGCCCGCGGAGTTCTCTGTGGCCCATGACCTTGGCGCTGGCTGTGCGCCGTGAGAGA 300  
Qy 356 TGATGACATGAGCAGACCCCGCTAGCATGAGACCGCTTGTGGCTGTGCTTCCGCGCA 415  
Db 301 TGATGACATGAGCAGACCCCGCTAGCATGAGACCGCTTGTGGCTGTGCTTCCGCGCA 360  
Qy 416 GCGCGCGCGCATCCGACGTCATGATCGTGGCCGAGCACTCAACCAAGATGGCCCGAG 475  
Db 361 GCGCGCGCGCATCCGACGTCATGATCGTGGCCGAGCACTCAACCAAGATGGCCCGAG 420  
Qy 476 CGCTTTCGCAAGGTCTACAGCAGATGCGGAGCCGCGCTACGATGTCTCATGAGGAGCT 535  
Db 421 CGCTTTCGCAAGGTCTACAGCAGATGCGGAGCCGCGCTACGATGTCTCATGAGGAGCT 480  
Qy 536 GCGCCACGAGAGAGGCTACTACCATATTCCTACTCGTGTGTGAGGGGCTGTGCAAGCA 595  
Db 481 GCGCCACGAGAGAGGCTACTACCATATTCCTACTCGTGTGTGAGGGGCTGTGCAAGCA 540  
Qy 596 TCGTGCCTGTCGATCTACATCCAGGCTGCCCACTACGCGCCAGGCC 645  
Db 541 TCGTGCCTGTCGATCTACATCCAGGTCGAGGCGGAGCCGACCGGCC 590

## RESULT 4

US-10-104-047-262  
; Sequence 262, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 262  
; LENGTH: 3050  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-047-262

Query Match 59.6%; Score 491; DB 17; Length 3050;  
Best Local Similarity 97.1%; Pred. No. 8.4e-127;  
Matches 500; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 131 GCTCAGCGTGGCGCGCGCTGTGCAAGCAGAGGTGTCCATCAGACGCTGGCCACCGATG 190  
Db 305 GCTCAGCGTGGCGCGCGCTGTGCAAGCAGAGGTGTCCATCAGACGCTGGCCACCGATG 364  
Qy 191 GCCCAGCAGACCCAGCCTTCCCTGCCAAGGCCAGAGCCGTGCTCCCAACCAGCA 250  
Db 365 GCCCAGCAGACCCAGCCTTCCCTGCCAAGGCCAGAGCCGTGCTCCCAACCAGCA 424  
Qy 251 GCGCGGGGAGATGTGTGTGTCGCAAGCTGTGATGACTGTCTCAACTGGGCGCGGAGTT 310  
Db 425 GCGCGGGGAGATGTGTGTGTCGCAAGCTGTGATGACTGTCTCAACTGGGCGCGGAGTT 484  
Qy 311 CTCTGTGGCCCATGACCTTCCGCTGGCTGTGCGCGCTGTGAGATGTATGACATGGCAG 370  
Db 485 CTCTGTGGCCCATGACCTTCCGCTGGCTGTGCGCGCTGTGAGATGTATGACATGGCAG 544  
Qy 371 CACCCCGCTACGACATGAGACCGCTTGTGGCTGTGCTTCCGCGCCAGCCCGCCAGTCCG 430  
Db 545 CACCCCGCTACGACATGAGACCGCTTGTGGCTGTGCTTCCGCGCCAGCCCGCCAGTCCG 604  
Qy 431 ACGTACATGATGTGGCGCGGCACTCACTCAACCAAGATGGCCCGCTTGGCAAGTCT 490  
Db 605 ACGTACATGATGTGGCGCGGCACTCACTCAACCAAGATGGCCCGCTTGGCAAGTCT 664  
Qy 491 ACGACAGATCCCGAGCCGCGCTACGTTGCTCCATGGGAGCTGCGCAACGAGAGAG 550  
Db 665 ACGACAGATCCCGAGCCGCGCTACGTTGCTCCATGGGAGCTGCGCAACGAGAGAG 724  
Qy 551 GCTACTACACTATTTCTACTCTGCTGTGTGAGGGGCTGCGACCGCATCTGTCCCGTGA 610  
Db 725 GCTACTACACTATTTCTACTCTGCTGTGTGAGGGGCTGCGACCGCATCTGTCCCGTGA 784  
Qy 611 TCTACATCCAGGCTGCCCACTACGCGCCAGGCC 645  
Db 785 TCTACATCCAGGTCGAGGCGGAGCCGACCGGCC 819

## RESULT 5

US-10-104-047-914  
; Sequence 914, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:

PRINTING DATE: 2001-01-12  
NUMBER OF SEQ ID NOS: 934

APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kairos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stoik, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
APPLICANT: Hural, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C24  
CURRENT APPLICATION NUMBER: US/09/780.669  
NUMBER OF SEQ ID NOS: 943  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 32  
LENGTH: 789  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(789)  
OTHER INFORMATION: n = A,T,C or G  
US-09-780-669-32

Query Match 46.7%; Score 384.6; DB 9; Length 789;  
Best Local Similarity 75.9%; Pred. No. 3.4e-97;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

141 GGGCCGCGCTGTGACGACAGGCTGCATCAGACGCTGACCAACCAATGCGCCCAAGCAG 200  
739 GGGGAGATGTGNNNAGANGNGTTTTCNTTAGANNNGCCCAACCGGGGCCGAAGG 680  
201 CACCCAGCTGCGCTGCAAGGCGACGCGTGGCTCCAAACCCAGACCGGGGCGA 260  
679 GGANCCANCTTGCCNCCAAAGNNAAGAGCGTGCTCCAAACCCAGANNAACGGGGGA 620  
261 GTATGTGTGCGCAAGCTGATGACTGT--CACTGGGCGCGCGGAGTTCTGTG 317  
619 GGATTTGGGGGCCAAGGGGGATGACTTTGTGAACCTGGGCCCGCGAGNTTTTGN 560  
318 G---CCCATGACCTTGGCGCTGCTGCGCGCTGCGGAGATGATGACATGGCAGC-A 372  
559 GGGCCNCAAGAACTTTTGGGTGNCCTGNTGNGCCGGAGAGTGTGANAATNGCAGCA 500  
373 CCCCCTACGACATGACCGCTTTGGCGTG--TCTTCCGCGCAAGCCCGCGCAGTCCG 430  
499 CCCCNNNAAGACATGANCCTGTTTGGGNGNTTTTGGGGCCAGCCCGGCGCAGTCTG 440  
431 ACCTGATGATGTGGCGCGGCACTACCAACAAGATGGCCCGCTTGGCAAGTCT 490  
439 A-GTNAATGATTTGTGCGNGNANNTAACAAGAGGGCCCGCAGNG-TTTGCAAGGTTT 382  
491 ACAGACGAGATGCGGAGCGCGCTACGTCGTCATGGGAGTGCSCCAACGAGAGAG 550  
381 AAGACAGATGCGGAGCGCGGANAAGTGTTCANAGGAGG-TGNGCAACGAGNGNG 323  
551 GCTACTACACTATTCTACTCGTGTGTGAGGGGCTGGACCGCATCGTGCCTGTGCA 610  
322 GGTAAACCACTATTCTTAATNGGTGTGAGGGAGTGCAACGCAATTGTGCGCGGAAA 263  
611 TCTACATCCGAGGCTGCCACCTACGCGCGGAGCGCTGCTCTAGGACATCTCTGACGCTGC 670  
262 TTNAATCCCGAGGGTCCACACNAGCGCAGGGCCCTGTATTANAGCATCTGTGACGTGC 203

671 AGAGAAATCAACGCGGAGCGAGGCTGCAGATCTGTGTAACGAGTAGCGCCGCC 730  
202 AGAGAAATCAACGCGGAGCGAGGCTGCANATTTGTGACCGAGTAGAGGCCGCCGCC 143  
731 GCCCGCGCGAGGCTGTGCGCTGTCTGTCCCAAGCTGCTTGTCTCCGTGAGTTGTC 790  
142 GCCCGCGCGAGGCTGTGCGCTGTCTGTCCCAAGCTGCTTGTCTCCGTGAGTTGTC 83  
791 AATAACCTGCGCTGGGCAAAAAAAAAAAAA 824  
82 AATAACCTGCGCTGGNAAAAAAAAAAAAA 49

RESULT 8  
US-09-030-606-32/C  
Sequence 32, Application US/09030606  
Patent No. US20020081580A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F

NUMBER OF SEQUENCES: 224  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030.606  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David U.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.428C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-030-606-32

Query Match 46.7%; Score 384.6; DB 9; Length 789;  
Best Local Similarity 75.9%; Pred. No. 3.4e-97;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

141 GGGCCGCGCTGTGACGACGAGGCTGCATCAGACGCTGACCAACCAATGCGCCCAAGCAG 200  
739 GGGGAGATGTGNNNAGANGNGTTTTCNTTAGANNNGCCCAACCGGGGCCGAAGG 680  
201 CACCCAGCTGCGCTGCAAGGCGACGCGTGGCTCCAAACCCAGACCGGGGCGA 260  
679 GGANCCANCTTGCCNCCAAAGNNAAGAGCGTGCTCCAAACCCAGANNAACGGGGGA 620  
261 GTATGTGTGCGCAAGCTGATGACTGT--CACTGGGCGCGCGGAGTTCTGTG 317  
619 GGATTTGGGGGCCAAGGGGGATGACTTTGTGAACCTGGGCCCGCGAGNTTTTGN 560  
318 G---CCCATGACCTTGGCGCTGCTGCGCGCTGCGGAGATGATGACATGGCAGC-A 372  
559 GGGCCNCAAGAACTTTTGGGTGNCCTGNTGNGCCGGAGAGTGTGANAATNGCAGCA 500

QY 373 CCGGCTACGACATGAGACCGCTTGGCGTG-TCCTCCGCGACGCGCCAGTCCG 430  
DB 499 CCGGNNAAAGACATGAGCCGGTTTGGGANGNTTTTGGGGCCAGCCGAGCTG 440  
QY 431 ACCTCATGATCGTGGCCGCGACACTCACCAAGATGCCCCAGCGCTTCCGAAGTCT 490  
DB 439 A-GTAAATGATTTGGCGGANGNANNTAAACAAAAGAGGCGCCAGNG-TTTGCAAGTTT 382  
QY 491 ACAGCAGATGCGGAGCGCGCTACGTGTCTCCATGGGAGACTCGGCAACGGAGAG 550  
DB 381 AAGACGAGATGCGGAGCGCGANAGTGTTCANAGGAG-TGAGCCAAAGGANG 323  
QY 551 GCTACTACACTATTCTTCTACTCGTGTGAGGGGCTGCGACCGCATCTGCGCTGACA 610  
DB 322 GGTAAACCACTATTCTTAATNGTGTGAGGGGTCGACCGCATTTGCGCGTGA 263  
QY 611 TCTACATCCAGGCTGCGCCACTAGAGCGAGGCGCTGCTACAGGATCTTGCAGTGC 670  
DB 262 TTAAATCCAGGCTGCGCCACTAGAGCGAGGCGCTGTTTANAGCATCTGCACTGC 203  
QY 671 AGAGGAAGATCAAGCGGAGCGGAGGCTGCAGATCTGTACCGAGTACGCGCGCC 730  
DB 202 AGAGGAANATCAAGCGGAGCGGAGGCTGCANATTTGTATCCGAGATAGGCGCGCC 143  
QY 731 GCGGCGCGGAGCGCTGTGCGCTGCTGTCCCGAGCTGTGTCTCCGTGAGGTTGC 790  
DB 142 GCGGCGCGGAGCGCTGTGCGCTGTGCTCCCGAGCTGNTGTCTCCGAGGTTGC 83  
QY 791 AATAAACCTGCGCTGCGGCAAAAAAAAAA 824  
DB 82 AATAAACCTGCGCTGCGGCAAAAAAAAAA 49

RESULT 9  
US-09-822-827-32/c  
; Sequence 32, Application US/09822827  
; Patent No. US2002081680A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.534C1  
; CURRENT APPLICATION NUMBER: US/09/822,827  
; CURRENT FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 982  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(789)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-822-827-32

Query Match 46.7%; Score 384.6; DB 9; Length 789;  
Best Local Similarity 75.9%; Pred. No. 3,4e-97;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;  
QY 141 GGGCCCGGCTGTGACAGCAGAGGTTCATCAGAGCGTGCCACCGATGCCCAAGCAG 200  
DB 739 GGGGAGATGAGNNAGANGNTTTCNTTAGANNNGGCCACCGGGGGCCGAGAGG 680  
QY 201 CACCCAGCTGCGCTGCAAGGCGAGCGGTGCTCCCAACCCAGACGCGGGGCGA 260  
DB 679 GAGNCANCTTGCNNCAAGANNAGAGCGTGGTTCCTCAAAACCCAGNANCGGGGGA 620  
QY 261 GATGTTGGTGGCAAGCTGATGACTCTG---CAACTGGGCGCGCGAGTTCTCTG 317  
DB 619 GATTTGGGGGCGCAAGGGGATGACTTTGTTGAAACTGGGNCGCCCGGAGNTTTTGN 560

QY 318 G----CCATGACTTGGGCTGTGCTGTGCGCGGTGAGATGATGACATGAGCAGC-A 372  
DB 559 GGGCCNCAAGAACTTTTGGGTTGNCCTGANTGNGCCCGGAGAGTATGNANATNGCAACAA 500  
QY 373 CCGGCTACGACATGAGACCGCTTGGCGTG--TCCTCCGCGACGCGCCGCGCAAGTCCG 430  
DB 499 CCGGNNAAAGACATGAGCCGGTTTGGGANGNTTTTGGGGCCAGCCGAGCTG 440  
QY 431 ACCTCATGATGTTGGCGGCACTCACTCAAGATGAGCCCGACTTCCGAAGTCT 490  
DB 439 A-GTAAATGATTTGGCGGANGNANNTAAACAAAAGAGGCGCCAGNG-TTTGCAAGTTT 382  
QY 491 ACAGCAGATGCGGAGCGCGCTACGTGTCTCCATGGGAGACTGCGCAACGGAGAG 550  
DB 381 AAGACGAGATGCGGAGCGCGANAGTGTTCANAGGAG-TGAGCCAAAGGANG 323  
QY 551 GCTACTACACTATTCTTCTACTCGTGTGAGGGGCTGCGACCGCATCTGCGCTGACA 610  
DB 322 GGTAAACCACTATTCTTAATNGTGTGAGGGGTCGACCGCATTTGCGCGTGA 263  
QY 611 TCTACATCCAGGCTGCGCCACTAGAGCGAGGCGCTGCTTACGCGCATCTGCACTGC 670  
DB 262 TTAAATCCAGGCTGCGCCACTAGAGCGAGGCGCTGTTTANAGCATCTGCACTGC 203  
QY 671 AGAGGAAGATCAAGCGGAGCGGAGGCTGCAGATCTGTGTAACGAGTACGCGCGCC 730  
DB 202 AGAGGAANATCAAGCGGAGCGGAGGCTGCANATTTGTATCCGAGTAGGCGCGCC 143  
QY 731 GCGGCGCGGAGCGCTGTGCGCTGCTGTCCCGAGCTGTGTCTCCGTGAGGTTGC 790  
DB 142 GCGGCGCGGAGCGCTGTGCGCTGTGCTCCCGAGCTGNTGTGTCTCCGAGGTTGC 83  
QY 791 AATAAACCTGCGCTGCGGCAAAAAAAAAA 824  
DB 82 AATAAACCTGCGCTGCGGCAAAAAAAAAA 49

RESULT 10  
US-09-115-453-32/c  
; Sequence 32, Application US/09115453B  
; Patent No. US2002090372A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND  
; FILE REFERENCE: 210121.427C4  
; CURRENT APPLICATION NUMBER: US/09/115,453B  
; CURRENT FILING DATE: 1998-07-14  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(789)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-115-453-32

Query Match 46.7%; Score 384.6; DB 9; Length 789;  
Best Local Similarity 75.9%; Pred. No. 3,4e-97;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;  
QY 141 GGGCCCGGCTGTGACAGCAGAGGTTCATCAGAGCGTGCCACCGATGCCCAAGCAG 200  
DB 739 GGGGAGATGAGNNAGANGNTTTCNTTAGANNNGGCCACCGGGGGCCGAGAGG 680  
QY 201 CACCCAGCTGCGCTGCAAGGCGAGCGGTGCTCCCAACCCAGACGCGGGGCGA 260  
DB 679 GAGNCANCTTGCNNCAAGANNAGAGCGTGGTTCCTCAAAACCCAGNANCGGGGGA 620

Qy 261 GTATGTGGTGGCCAAAGCTGATGACTCTGT---CAACTGGGCGCGCCGAGTCTCTGTG 317  
Db 619 GGATTTGGGGGCAAGGGGATGACTTTGTGAACCTGGGNCCTCCCGAGNTTTTTTGN 560  
Qy 318 G----CCCATGACCTTGGGCTGGCTGCTGCGCCGTTGAGATGATGACATGGCAGC-A 372  
Db 559 GGGCCNCAAGAACTTTTGGGTTGNCCTGNTGNCCTGGAGAGTGATGANAATNACAGAA 500  
Qy 373 CCCCCTACGACATGAGACCGCTTTGGGCTGG--TCTTCGGGCGCAGCCGCGCAGTCCG 430  
Db 499 CCCCNNAAAGACATGNCCTGGTTTGGGAGNNTTTTTTGGGCGCAGCCCGNCCAGTCTG 440  
Qy 431 ACCTCATGATGCTGGCCGCGCACTCAACAAGATGGCCCGACGCTTTCGCAAGTCT 490  
Db 439 A-GTNAATGATTTGTGGCNGNANNTAACAAGAGGCGCCAGNG-TTTCGCAAGTCT 382  
Qy 491 ACGACCAAGATGCGGAGCGCGCTACGTTCTCCTAGTGGAGTCTGCCCAACGAGAG 550  
Db 381 AAGACCAAGATGCGGAGCGCGAGAGGTTTCCANAGGAG-TGNGCCCAACGAGNG 323  
Qy 551 GCTACTACCACTATTCTCTACTCGGTGGTGGAGGGGCTGGACCGGATCGTGGCGTGA 610  
Db 322 GGTAAACCACTATTCTCTAATNGTGTGAGGGAGTGGACCGCATTTGTGCCGTGAA 263  
Qy 611 TCTACATCCAGGCTGCCCACTACGGCCGAGGCTGCTCTACGCGCATCTCTGACGTGC 670  
Db 262 TTNAATATCCAGGGTGGCCCAACNANNGCGAGGCTGTGTTTANAGCATCTCTGACGTGC 203  
Qy 671 AGAGGAAGATCAACCGGAGCGGAGGCTGCAGATCTGTGATCCGCAAGTACGCGCGCC 730  
Db 202 AGAGGAANATCAACCGGAGCGGAGGCTGCANATTTGTGTACCGCAGCTAAGGCGCGCC 143  
Qy 731 GCGCGCGCGGAGGCTGCGCGCTGTCTGCCAGCCTGTGTGTCCCGTGAAGTGTGC 790  
Db 142 GCGCGCGCGGAGGCTGTGCTGTCTGCCAGCCTGTGTGTGTCTCCGAGAGTGTGC 83  
Qy 791 AATAAACCCTGCTCGGCAAAAAAAAAAAAA 824  
Db 82 AATAAACCCTGCTCGGCAAAAAAAAAAAAA 49

RESULT 11  
US-09-232-880-32/C  
/ Sequence 32, Application US/09232880  
/ Publication No. US20020182596A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Xu, Jianshun  
/ APPLICANT: Dillon, David C.  
/ APPLICANT: Mitcham, Jennifer Lynn  
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF  
/ FILE REFERENCE: 210121.428C6  
/ CURRENT APPLICATION NUMBER: US/09/232, 880  
/ NUMBER OF SEQ ID NOS: 338  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 32  
/ LENGTH: 789  
/ TYPE: DNA  
/ ORGANISM: Homo sapien  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ LOCATION: (1)-(789)  
/ OTHER INFORMATION: n = A,T,C or G  
US-09-232-880-32

Query Match 46.7%; Score 384.6; DB 9; Length 789;  
Best Local Similarity 75.9%; Pred. No. 3.4e-97;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;  
Qy 141 GGGCCCCGCTGTGCAGCAGCAGGTGTCATCAAGCTGCGCCACCGATGSCCAAGCAG 200  
Db 739 GGGGGAATGTGNNNAGANNGNTTTCTTATGAGNNGGCCCAACGGGGCCGAAGAGG 680

Qy 201 CACCAGCTGCTCTGCGCAAGGCCAGACCGTGGCTCCCAAAACCAAGACCGGGCGCA 260  
Db 679 GGANCCANCTTGGCCNNCAAGNAGAGCGCTGGGTTCCAAACCCAGNANCGGGGGA 620  
Qy 261 GTATGTGGTGGCCAAAGCTGATGACTCTGT---CAACTGGGCGCGCCGAGTCTCTGTG 317  
Db 619 GGATTTGGGGGCAAGGGGATGACTTTGTGAACCTGGGNCCTCCCGAGNNTTTTTTGN 560  
Qy 318 G----CCCATGACCTTGGGCTGGCTGCTGCGCCGTTGAGATGATGACATGGCAGC-A 372  
Db 559 GGGCCNCAAGAACTTTTGGGTTGNCCTGNTGNCCTGGAGAGTGATGANAATNACAGAA 500  
Qy 373 CCCCCTACGACATGAGACCGCTTTGGGCTGG--TCTTCGGGCGCAGCCGCGCAGTCCG 430  
Db 499 CCCCNNAAAGACATGNCCTGGTTTGGGAGNNTTTTTTGGGCGCAGCCCGNCCAGTCTG 440  
Qy 431 ACCTCATGATGCTGGCCGCGCACTCAACAAGATGGCCCGACGCTTTCGCAAGTCT 490  
Db 439 A-GTNAATGATTTGTGGCNGNANNTAACAAGAGGCGCCAGNG-TTTCGCAAGTCT 382  
Qy 491 ACGACCAAGATGCGGAGCGCGCTACGTTCTCCTAGTGGAGTCTGCCCAACGAGAG 550  
Db 381 AAGACCAAGATGCGGAGCGCGAGAGGTTTCCANAGGAG-TGNGCCCAACGAGNG 323  
Qy 551 GCTACTACCACTATTCTCTACTCGGTGGTGGAGGGGCTGCGACCGCATCGTGGCGTGA 610  
Db 322 GGTAAACCACTATTCTCTAATNGTGTGAGGGAGTGGACCGCATTTGTGCCGTGAA 263  
Qy 611 TCTACATCCAGGCTGCCCACTACGGCCGAGGCTGCTCTACGCGCATCTCTGACGTGC 670  
Db 262 TTNAATATCCAGGGTGGCCCAACNANNGCGAGGCTGTGTTTANAGCATCTCTGACGTGC 203  
Qy 671 AGAGGAAGATCAACCGGAGCGGAGGCTGCAGATCTGTGATCCGCAAGTACGCGCGCC 730  
Db 202 AGAGGAANATCAACCGGAGCGGAGGCTGCANATTTGTGTACCGCAGCTAAGGCGCGCC 143  
Qy 731 GCGCGCGCGGAGGCTGCGCGCTGTCTGCCAGCCTGTGTGTCCCGTGAAGTGTGC 790  
Db 142 GCGCGCGCGGAGGCTGTGCTGTCTGCCAGCCTGTGTGTGTCTCCGAGAGTGTGC 83  
Qy 791 AATAAACCCTGCTCGGCAAAAAAAAAAAAA 824  
Db 82 AATAAACCCTGCTCGGCAAAAAAAAAAAAA 49

RESULT 12  
US-09-895-793-32/C  
/ Sequence 32, Application US/09895793  
/ Publication No. US20020192763A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Xu, Jianshun  
/ APPLICANT: Dillon, David C.  
/ APPLICANT: Mitcham, Jennifer L.  
/ APPLICANT: Harlocker, Susan L.  
/ APPLICANT: Jiansun, Yudi  
/ APPLICANT: Kalos, Michael D.  
/ APPLICANT: Ketter, Marc W.  
/ APPLICANT: Stoik, John A.  
/ APPLICANT: Day, Craig H.  
/ APPLICANT: Vedvick, Thomas S.  
/ APPLICANT: Carter, Derrick  
/ APPLICANT: Li, Samuel X.  
/ APPLICANT: Wang, Aijun  
/ APPLICANT: Skeiky, Yasir A.W.  
/ APPLICANT: Hepley, William T.  
/ APPLICANT: Henderson, Robert A.  
/ APPLICANT: Hural, John  
/ APPLICANT: McNeill, Patricia D.  
/ APPLICANT: Houghton, Raymond L.  
/ APPLICANT: Vinals de Baesols, Carlota  
/ APPLICANT: Foy, Teresa  
/ APPLICANT: Fanger, Gary R.

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-793-32

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Query Match      46.7%; Score 384.6; DB 9; Length 789;
Best Local Similarity 75.9%; Pred. No. 3.4e-97;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

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QY 141 GGGCCCGGCTGTGACGACGAGTGTCCATCAGACCGTGGCCACCGATGGCCCAAGCAG 200
DB 739 GGGGATGTGTGNNNAGANGGTTTCTTATGAGNNGGCCACCGGGGCCGAGAGG 680
QY 201 CACCCAGCTGCTGCTGCCAAGGCGAAGCCGTGCTCCAAACCCAGACCGGGGCGA 260
DB 679 GGANCCANCTTCCNNCCAAAGNAGAGCGGTGCTCCAAACCCAGNANCCGGGGGA 620
QY 261 GTATGTGTGGCCCAAGTGTGACCTGT---CAACTGGGCGCCCGGAGTTCTCTGTG 317
DB 619 GGATTTGGGGGCGCAAGGGGAGTACTTGTGTAACTGGAGCCCGCCGAGNTTTTTGN 560
QY 318 G----CCCATGACCTTGGCGCTGCGCTGCGCGGTGAGATGATGACATGGCAGC-A 372
DB 559 GGGCCNCAAGAACTTTGGGTGNCCTGNTGNGCCCGGAGATGATGANAATNGCAGCA 500
QY 373 CCGGCTACGACATGTGACCGCTTTGGCGTG--TCTTCGCGCCAGCCCGGCGCATGCG 430
DB 499 CCGGNNNAGACATGTGNCGGTGTGGGNGNTTTTTGGGGCGCAGCCCGNCGACGTG 440
QY 431 ACATCATGATGTGGCGCGGACACTCACCAACAAGTGGCCCGGCTTCCGCAAGGCTCT 490
DB 439 A-GTNATGATGTGGCNGNANNTAAACCAAAAGAGGCCCGCCAGNG-TTGGCAAGGTTT 382
QY 491 ACGACCATATGCGGAGCGCGCTACGTGTCTCATGTGGGAGCTGCGCAACGAGAG 550
DB 381 AAGACCATATGCGGAGCGCGANAGTGTGTTCCANGGGAG-TGNGCCAAACGNGG 323
QY 551 GCTACTACCACTATTTCTACTCGGTGTGAGGGGCTGCGACCGCATCTGCGGTGACA 610
DB 322 GGTAAACCACTATTTCTAATGAGTGTGAGGGGNTGCGACCGCATTTGTCCTGTA 263
QY 611 TCTACATCCAGAGCTGCGCACTACGCGGAGGCGCTGCTACGCGATCTTGAAGTGC 670
DB 262 TTNAATATCCAGAGGTGCGCAACNANNGCCGAGGCGCTTTTANAGGATCTTCAAGTGC 203
QY 671 AGAGAGATATCAAGCGGAGCGAGCGTGTGATCTGTATCCGAGGTAGCGCGCGCC 730
DB 202 AGAGAGATATCAAGCGGAGCGAGCGTGTGATCTGTATCCGAGGTAGCGCGCGCC 143
QY 731 GCGGCGCGGAGCGCTGTGCGCGCTGTGCTCCAGAGCTGTGTCCTCTAGGTTGTC 790
DB 142 GCGGCGCGGAGCGCTGTGCGCGCTGTGCTCCAGAGCTGTGTCCTCTAGGTTGTC 83
QY 791 AATTAACCTGCTTGGGCAAAAAAAAAAAAAA 824
DB 82 AATTAACCTGCTTGGGCAAAAAAAAAAAAAA 49

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RESULT 13
US-09-895-814-32/c
; Sequence 32; Application US/09895814

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; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Ketter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-814-32

```

```

Query Match      46.7%; Score 384.6; DB 9; Length 789;
Best Local Similarity 75.9%; Pred. No. 3.4e-97;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

```

```

QY 141 GGGCCCGGCTGTGACGACGAGTGTCCATCAGACCGTGGCCACCGATGGCCCAAGCAG 200
DB 739 GGGGATGTGTGNNNAGANGGTTTCTTATGAGNNGGCCACCGGGGCCGAGAGG 680
QY 201 CACCCAGCTGCTGCTGCCAAGGCGAAGCCGTGCTCCAAACCCAGACCGGGGCGA 260
DB 679 GGANCCANCTTCCNNCCAAAGNAGAGCGGTGCTCCAAACCCAGNANCCGGGGGA 620
QY 261 GTATGTGTGGCGCAAGCTGTGATGACCTGT---CAACTGGGCGCCCGGAGTTCTGTG 317
DB 619 GGATTTGGGGGCGCAAGGGGAGTGACTTGTGTAACTGGAGCCCGCCGAGNTTTTTGN 560
QY 318 G----CCCATGACCTTGGCGCTGCGCTGCGCGGTGAGATGATGACATGGCAGC-A 372
DB 559 GGGCCNCAAGAACTTTGGGTGNCCTGNTGNGCCCGGAGATGATGANAATNGCAGCA 500
QY 551 GCTACTACCACTATTTCTACTCGGTGTGAGGGGCTGCGACCGCATCTTGAAGTGC 670
DB 262 TTNAATATCCAGAGGTGCGCAACNANNGCCGAGGCGCTTTTANAGGATCTTCAAGTGC 203
QY 671 AGAGAGATATCAAGCGGAGCGAGCGTGTGATCTGTATCCGAGGTAGCGCGCGCC 730
DB 202 AGAGAGATATCAAGCGGAGCGAGCGTGTGATCTGTATCCGAGGTAGCGCGCGCC 143
QY 731 GCGGCGCGGAGCGCTGTGCGCGCTGTGCTCCAGAGCTGTGTCCTCTAGGTTGTC 790
DB 142 GCGGCGCGGAGCGCTGTGCGCGCTGTGCTCCAGAGCTGTGTCCTCTAGGTTGTC 83
QY 791 AATTAACCTGCTTGGGCAAAAAAAAAAAAAA 824
DB 82 AATTAACCTGCTTGGGCAAAAAAAAAAAAAA 49
QY 491 ACGACCATATGCGGAGCGCGCTACGTGTGTCCATGTGGGAGCTGCGCAACGAGAGAG 550
DB 381 AAGACCATATGCGGAGCGCGANAGTGTGTTCCANGGGAG-TGNGCCAAACGNGG 323

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Qy 551 GCTACTACACTATTCCTACTCGGTGTGTAGAGGGCTCGCAGCGCATCTGCGCCGTGACA 610
    |||
Db 322 GGTAAACCACTATTCTCAATNGGTGGTGAAGGGGTGGAGCCGATTGTGCCCGTGGAAA 263
Qy 611 TCTACATCCAGGCTGCCCACTACGCGCGAGCCCTGCTTACGGCATCTCTGCACTGC 670
    |||
Db 262 TTNAAATCCCGGGTGGCCACCCANNGCCGAGGCCCTGTTTANNGCATCTCTGCACTGC 203
Qy 671 AGAGAAAGATCAAGCGGAGGAGGAGGCTGCATCTGTACCGCAGTACGCGCGCGCC 730
    |||
Db 202 AGAGAAANATCAAGCGGAGGAGGAGGCTGCANATTGTGTACCGCAGTACGCGCGCC 143
Qy 731 GCCCGCGCGGAGGCTGTGCGCGCTCTGTCCCGCAGCCTGCTTGTCTCCGTGAGGTTGTC 790
    |||
Db 142 GCCCGCGCGGAGGCTGTGCGCGCTCTGTCCCGCAGCCTGTTGTGTCTCCGAGGTTGTC 83
Qy 791 AATAAACCTGCGCTCGGCAAAAAA 824
    |||
Db 82 AATAAACCTGCGCTTNGNAAAAA 49
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## RESULT 14

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US-10-012-896-32/c
; Sequence 32, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kaios, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Jasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Babsois, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 65, 68, 92, 103, 171, 195, 219, 238, 240, 260, 288, 301,
; LOCATION: 317, 324, 327, 336, 345, 358, 395, 417, 419, 421, 424, 436,
; LOCATION: 449, 468, 470, 483, 493, 494, 507, 510, 512, 528, 531, 536,
; LOCATION: 554, 560, 568, 579, 628, 631, 656, 657, 664, 665, 672
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: 676, 703, 704, 711, 718, 721, 726, 727, 728, 741, 742, 744,
; LOCATION: 745, 749, 753, 757, 759, 773, 787
; OTHER INFORMATION: n = A,T,C or G
US-10-012-896-32
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Query Match 46.7%; Score 384.6; DB 13; Length 789;  
Best Local Similarity 75.9%; Pred. No. 3.4e-97;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

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Db 739 GGGGATGTGTNNNANAGANGNGTTCCTTAGAGNNNGGCCACCGGGGGCCGAAGG 680
Qy 201 CACCCAGCTGCTCCGCAAGGCCAAGCCGTGGCTCCCAAACCCAGACGCGGGCGCA 260
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Db 679 GGANCCANCTTGCCNNCCAAAGNNAAGCGGTGGCTCCAAACCCAAANAAACGGGGGA 620
Qy 261 GTATGTGTGSCCAAGCTGATGACTCTGT---CAACTGGGCGCGCGGAGTTCTGTG 317
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Db 619 GGATTTGGGGSCCAAGGGGAGTACTTGTGTGAAACTGGAGCCCGCGAGTTTGTGN 560
Qy 318 G----CCCATGACCTTGCGGCTGTGCTGCGCGCGTGGAGATGATGACATGGCAGC-A 372
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Db 559 GGGCCNCAAGAACTTTGTGGTTGNCCTGTGTGNGCCCGGAGAGTGTGATGNANATNGCAGCA 500
Qy 373 CCCCCCTACGACATGAGACCCCTTTGGCGTGG--TCTTCCGGCCAGCCCGCCAGTCCG 430
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Db 499 CCGCGNNAAGACATGAGNCCGGTTTGGGNGNTTTTGGGGCCAGCCCGCCAGTCTG 440
Qy 431 ACGTCATGATGTGGCGCGGACACTCACCAACAAGATGGCCCGCGCTTGCGAAGTCT 490
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Db 439 A-GTNATGATTTGTGCGNGNANATTAACCAAAAGAGGCCCAAG--TTTGCAAGTTT 382
Qy 491 ACGACAGATGCGGAGCGCGCTACGTGTCTCCATGGGAGCTGCGCCAAAGAGAG 550
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Db 381 AAGACAGATGCGGAGCGCGGANAAGTGTTCANGGGAG--TGNCCAAAGGNGG 323
Qy 551 GCTACTACACTATTCTCACTCGGTGTGAGGGGCTGCGACCGCATCTGTCCTGTGACA 610
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Db 322 GGTAAACCACTATTCTCAATNGGTGGTGAAGGGGTGGAACCGCATTTGTGCCGTGAAA 263
Qy 611 TCTACATCCAGGCTGCCCACTACGCGGAGGCGCTGCTCAAGGCACTCTGCACTGC 670
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Db 262 TTNAAATCCCGGGTGGCCACCCANNGCCGAGGCCCTGTTTANNGCATCTCTGCACTGC 203
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Db 202 AGAGAAANATCAAGCGGAGGAGGCTGCANATTGTGTACCGCAGTACGCGCGCGCC 143
Qy 731 GCCCGCGCGGAGGCTGTGCGCGCTCTGTCCCGCAGCCTGCTTGTCTCCGTGAGGTTGTC 790
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Db 142 GCCCGCGCGGAGGCTGTGCGCGCTCTGTCCCGCAGCCTGTTGTCTCCGAGGTTGTC 83
Qy 791 AATAAACCTGCGCTCGGCAAAAAA 824
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Db 82 AATAAACCTGCGCTTNGNAAAAA 49
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## RESULT 15

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US-10-010-940-32/c
; Sequence 32, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kaios, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2005, 22:32:18 ; Search time 190 Seconds  
(without alignment)  
7096.274 Million cell updates/sec

Title: US-09-525-867-9  
Perfect score: 824  
Sequence: 1 cggctcgagcgctcgagcg.....cggcaaaaaaaaaaaaaa 824

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 240568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
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6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	750.8	91.1	772	4	US-09-620-312D-670 Sequence 670, App
2	384.6	46.7	789	3	US-09-020-956-32 Sequence 32, Appl
3	384.6	46.7	789	3	US-09-030-607-32 Sequence 32, Appl
4	384.6	46.7	789	3	US-09-439-313-32 Sequence 32, Appl
5	384.6	46.7	789	3	US-09-352-616A-32 Sequence 32, Appl
6	384.6	46.7	789	3	US-09-232-149A-32 Sequence 32, Appl
7	384.6	46.7	789	4	US-09-159-812-32 Sequence 32, Appl
8	384.6	46.7	789	4	US-09-636-215-32 Sequence 32, Appl
9	384.6	46.7	789	4	US-09-685-166A-32 Sequence 32, Appl
10	384.6	46.7	789	4	US-09-115-453-32 Sequence 32, Appl
11	384.6	46.7	789	4	US-09-688-489-32 Sequence 32, Appl
12	384.6	46.7	789	4	US-09-679-426-32 Sequence 32, Appl
13	384.6	46.7	789	4	US-09-759-143-32 Sequence 32, Appl
14	384.6	46.7	789	4	US-09-651-236-32 Sequence 32, Appl
15	277.6	33.7	2378	4	US-09-270-767-14895 Sequence 14895, A
16	236.8	28.7	275	4	US-09-313-294A-6583 Sequence 6583, Ap
17	161.4	19.6	666	4	US-09-252-991A-15142 Sequence 15142, A
18	161.4	19.6	966	4	US-09-252-991A-14622 Sequence 14622, A
19	152	18.4	4403765	3	US-09-103-840A-2 Sequence 2, Appl
20	152	18.4	4411529	3	US-09-103-840A-1 Sequence 1, Appl
21	143.2	17.4	513	4	US-09-902-540-4615 Sequence 4615, Ap
22	143.2	17.4	27490	4	US-09-902-540-1227 Sequence 1227, Ap
23	127.2	15.4	690	4	US-09-489-039A-5374 Sequence 5374, Ap
24	119.6	14.5	615	4	US-09-248-796A-2829 Sequence 2829, Ap
25	112.2	13.6	58909	4	US-09-596-002-30 Sequence 30, Appl
26	110.2	13.4	708	4	US-09-540-236-467 Sequence 467, App
27	92.8	11.3	798	4	US-09-489-039A-2763 Sequence 2763, Ap

28	92	11.2	735	4	US-09-543-681A-43 Sequence 43, Appl
29	79	9.6	684	4	US-09-328-352-581 Sequence 581, App
30	79	9.6	640681	4	US-09-790-988-1 Sequence 1, Appl
31	52.4	6.4	2322	4	US-09-476-242-20 Sequence 20, Appl
32	52.4	6.4	2541	4	US-09-476-242-9 Sequence 9, Appl
33	52.4	6.4	2541	4	US-09-476-242-11 Sequence 11, Appl
34	50.8	6.2	2322	4	US-09-476-242-18 Sequence 18, Appl
35	50.8	6.2	2352	4	US-09-476-242-26 Sequence 26, Appl
36	50.8	6.2	2541	4	US-09-476-242-10 Sequence 10, Appl
37	49.2	6.0	2322	4	US-09-476-242-19 Sequence 19, Appl
38	49.2	6.0	2541	4	US-09-476-242-12 Sequence 12, Appl
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44	47.4	5.8	1968	4	US-09-252-991A-1231 Sequence 1231, Ap
45	47.4	5.8	17726	4	US-09-902-540-1148 Sequence 1148, Ap

## ALIGNMENTS

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RESULT 1
US-09-620-312D-670
; Sequence 670, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Yanod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Ruihong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radjoe T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pf_fl_genes Version 1.0
; SEQ ID NO 670
; LENGTH: 772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (24) .. (665)
US-09-620-312D-670
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Query Match 91.1%; Score 750.8; DB 4; Length 772;
Best Local Similarity 99.1%; Pred. No. 3.9e-165;
Matches 755; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
CY 63 GAAGCGGAGGCGCAAGATGGCGGTGCTGACGCTCTGCGGCGGCTTCGAGATCCT 122
DB 8 GAAGCGGAGGCGCAAGATGGCGGTGCTGCTGCTGCTGCGGCGGCTTCGAGATCCT 67
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DB 68 TGGTCTGCGCTTCAGCGTGGGCGCGCTGTGTGAGGACAGAGGTGTCATGAGAGCTGGC 127
QY 183 CACCGATGGCCCAACAGACCCAGAGCTGGCCCTTGCAGAAAGCCAGAGCCGTGTGCTCCAA 242
DB 128 CACCGATGGCCCAACAGACCCAGAGCTGGCCCTTGCAGAAAGCCAGAGCCGTGTGCTCCAA 187
QY 243 ACCGAGAGCCGGGGCGAGTATGTGTGTGGCCAGAGCTGGATGACTGCTCAACTGGGGCCG 302
DB 188 ACCGAGAGCCGGGGCGAGTATGTGTGTGGCCAGAGCTGGATGACTGCTCAACTGGGGCCG 247
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DB 308 CATGGCAGACCCCGCTACGACATGAGACCGCTTGGGGGTGTCTTCCGGCCAGCCCGCG 367
QY 423 CCAGTCCGAGCTCATGATCGTGGCCGAGCACTACCAACAGAGTGGCCCGAGCGCTTGG 482
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QY 483 CAAGTCTACGACCAAGTGGCGGAGCGCTACGCTGTCTCATGGGAGCTGGCCAA 542
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QY 783 AGGTGTCAATAAAGCTGCTCGGGCAAAAAA 824
DB 728 AGGTGTCAATAAAGCTGCTCGGGCTGCGCGCAAAAAA 769

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RESULT 2  
 US-09-020-956-32/C  
 ; Sequence 32, Application US/09020956  
 ; Patent No. 6261562  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillan, Davin C.  
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
 ; NUMBER OF SEQUENCES: 178  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEED AND BERRY LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/020,956  
 ; FILING DATE: 09-FEB-1998

CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mark David J.  
 ; REGISTRATION NUMBER: 31,392  
 ; REFERENCE/DOCKET NUMBER: 210121.427C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 32:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 789 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-09-020-956-32

Query Match 46.7%; Score 384.6; DB 3; Length 789;  
 Best Local Similarity 75.9%; Pred. No. 4,2e-80;  
 Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

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QY 141 GGGCCCGCTGTGAGGACGAGGTGTCATGAGCGTGGGCCAGATGGCCAGACG 200
DB 739 GGGGAGATGTGNNNAGANGNGTTTCTTGTAGAGNNGGCCACCGGGGGCCAGAGG 680
QY 201 CACCCAGCTTCGCTGCCAAAGCCAGAGCCGTGGCTCCAAACCCAGAGCCGGGCGA 260
DB 679 GAANCAACTTGGCCNCAAGANNAGAGCGTGGGTTCCAAACCAAGAAACGGGGGA 620
QY 261 GTATGTGTGGCCAACTGATGACTGTGCT---CAACTGGGCGCCCGAGTTCTGTG 317
DB 619 GATTTGGGGGCCAAGGGGATGACTTGTGTAACGTGGANCCCGGAGTTTTTTGN 560
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QY 373 CCGCGCTACGACATGAGACCGCTTTGGCGTGG--TCTTCGCGCCAGCCCGCGCATGCG 430
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QY 431 AGCTCATGTGCTGTGCGCGGCACTACACAAAGATGGCCCGAGCTTGTGCAAGTCT 490
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QY 791 AATAAAGCTGCTCGGGCAAAAAA 824
DB 82 AATAAAGCTGCTCGGGCAAAAAA 49

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RESULT 3  
 US-09-030-607-32/C  
 ; Sequence 32, Application US/09030607

Patent No. 6262245  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, David C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
NUMBER OF SEQUENCES: 224  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030.607  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.427C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-030-607-32

Query Match 46.7%; Score 384.6; DB 3; Length 789;

Best Local Similarity 75.9%; Pred. No. 4.2e-80;

Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

Qy 141 GGGCCGCGCTGTGCAGCAGGCTGCATCAGAGCGTGGCCACCGATGGCCCAAGCAG 200  
Db 739 GGGGAGTGTGNNAGANGNGTTTNTTAGANNNGGCCACCGGGGCCGAAGG 680  
Qy 201 CACCCAGCTTGCCTGCAAGGCCAGAGCGGTGCTCCAAACCCAGACCGGGGCGA 260  
Db 679 GGANCCANCTTGCNNCCAAAGNAGAGCGGTGCTCCAAACCCAGNANCGGGGGA 620  
Qy 261 GTATGTGTGGCAAGCTGTGATGACTGTG---CACTGGGCGCGCGAGTTCTCTGTG 317  
Db 619 GGAATTTGGGGCCAAAGGGAGTGAATTTGTGAACCTGGAGNCCCCCGAGNTTTTTGN 560  
Qy 318 G----CCCATGACCTTGCCTGCTGCTGCTGCGCGGTGAGATGATGACATGGCAGC-A 372  
Db 559 GGGCGNCAAGAACTTTGGGTGNCCTGNTGNGCCCGGAGGTATGAAATNGAGCAA 500  
Qy 373 CCGCGCTAAGCATGAGACCGCTTTGGCGTG--TCTTCGCGCCAGCCCGCGCATCTCG 430  
Db 499 CCGCGNNAAGACATGAGNCGGTTTGGGAGNATTTTTTGGGGCCAGCCCGNCCAGTCTG 440  
Qy 431 AGCTCATGATGTGGCGGGCACTCACCACCAAGATGGCCCGCGGTGGCAAGTCT 490  
Db 439 A-GTNATGATTTGTGCGNNGNANNTTAACCAAAAGAGGCCCAANG-TTTGCAAGGTTT 382  
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Qy 551 GCTACTACCACTATTCTACTCGGTGTGAGGGGCTGCGACCGCATGCTGCCCGTGGCA 610  
Db 322 GGTAAACACTATTCTTAATGAGTGTGAGGGGAGTGGACCGCATGTGTGCCCGGTGAAA 263

RESULT 4  
US-09-439-313-32/C  
Sequence 32. Application US/09439313

Patent No. 629505  
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, David C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan Louise

APPLICANT: Jiang Yuqi

APPLICANT: Reed, Steven G.

APPLICANT: Kalos, Michael

APPLICANT: Fanger, Gary

APPLICANT: Retter, Mark

APPLICANT: Solk, John

APPLICANT: Day, Craig

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

FILE REFERENCE: 210121.427C9

CURRENT APPLICATION NUMBER: US/09/439.313

NUMBER OF SEQ ID NOS: 575

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 32

LENGTH: 789

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)..(789)

OTHER INFORMATION: n = A,T,C or G

US-09-439-313-32

Query Match 46.7%; Score 384.6; DB 3; Length 789;

Best Local Similarity 75.9%; Pred. No. 4.2e-80;

Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

Qy 141 GGGCCGCGCTGTGCAGCAGGCTGCATCAGAGCGTGGCCACCGATGGCCCAAGCAG 200  
Db 739 GGGGAGTGTGNNAGANGNGTTTNTTAGANNNGGCCACCGGGGCCGAAGG 680  
Qy 201 CACCCAGCTTGCCTGCAAGGCCAGAGCGGTGCTCCAAACCCAGACCGGGGCGA 260  
Db 679 GGANCCANCTTGCNNCCAAAGNAGAGCGGTGCTCCAAACCCAGNANCGGGGGA 620  
Qy 261 GTATGTGTGGCAAGCTGTGATGACTGTG---CACTGGGCGCGCGAGTTCTCTGTG 317  
Db 619 GGAATTTGGGGCCAAAGGGAGTGAATTTGTGAACCTGGAGNCCCCCGAGNTTTTTGN 560  
Qy 318 G----CCCATGACCTTGCCTGCTGCTGCTGCGCGGTGAGATGATGACATGGCAGC-A 372  
Db 559 GGGCGNCAAGAACTTTGGGTGNCCTGNTGNGCCCGGAGGTATGAAATNGAGCAA 500  
Qy 373 CCGCGCTAAGCATGAGACCGCTTTGGCGTG--TCTTCGCGCCAGCCCGCGCATCTCG 430

Db 499 CCCGNNAGACATGANCCTGTTTGGGNGNTTTTGGGGCCAGCCCGACAGTCTG 440  
QY 431 ACCTCATGATCGTGGCCGACACTCACCAAGATGCGCCAGCGCTTCCAGTCT 490  
Db 439 A-GTNAATGATGTGGGNGNANNTAACCAAAAGAGGCCAGNG-TTTCGAAGTTT 382  
QY 491 AGCAGCAGATGCCGAGCGCGCTACGTGTCTCCATGGGAGACTGCGCAACGAGAG 550  
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QY 551 GCTACTACACTATTCCTACTGCTGTGAGGAGGCTGCGACCGCATCGTCCGTGACA 610  
Db 322 GGTAAACCACTATTCCTAATNGGTGTAGGGGNTGCCACTTGTGCCCGGAGAA 263  
QY 611 TCTACATCCAGGCTGCCCACTACGCGCGAGCCCTGTCTACGCGCATCTGACGCTGC 670  
Db 262 TTNAATCCAGGCTGCCCAACNANGCGAGGCCCTGTTTTANGCATCTGACGCTGC 203  
QY 671 AAGAGAAATCAAGCGGAGCGGAGCTGCANATTTGGTACCGCAGGTAGGGCCGCC 143  
Db 202 AAGAGAAATCAAGCGGAGCGGAGCTGCANATTTGGTACCGCAGGTAGGGCCGCC 143  
QY 731 GCCGCGCGGAGCGCTGTGCGCGCTGCTGCCAGCGCTGTGTCCCGTAGAGTTGTC 790  
Db 142 GCCGCGCGGAGCGCTGTGCGCGCTGCTGCCAGCGCTGTGTGTCCCGTAGAGTTGTC 83  
QY 791 AATAAAGCTGCGCTGCGGCAAAAAA 824  
Db 82 AATAAAGCTGCGCTGCGGCAAAAAA 49

RESULT 5  
US-09-352-616A-32/c  
; Sequence 32, Application US/09352616A  
; Patent No. 6395278  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, David C.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
; FILE REFERENCE: 210121.427C8  
; CURRENT APPLICATION NUMBER: US/09/352.616A  
; CURRENT FILING DATE: 1999-07-13  
; NUMBER OF SEQ ID NOS: 472  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(789)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-352-616A-32

Query Match 46.7%; Score 384.6; DB 3; Length 789;  
Best Local Similarity 75.9%; Pred. No. 4.2e-80;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;  
QY 141 GGGCGCGCTGTGACGACGAGGTGTCCATCAGAGCGTGCCACCGATGCGCCAAAGCAG 200  
Db 739 GGGGAGATGTGNNAGANGNGTTTCTTAGAGNNGGGCCACCGGGGCCCGAAGGG 680  
QY 201 CACCCAGCTGCTGTGCAAGGCGAGCGTGCTCCAAACCGACGCGGGCGCA 260  
Db 679 GAGNCANCTTGCNNCCAAAGGAGCGGTGCTCCAAACCGACGAGGCGGAG 620  
QY 261 GTATGTGTGCGCAAGCTGTGATGCTCGT---CACTGGCGCGCGGAGTTCTCTGTG 317  
Db 619 GGAATTTGGGGCGCAAGGAGATGATCTTTGTGAAACTGGGNCCTCCCGAGAGTTTTCN 560

QY 318 G-----CCATACCTTTGGCGCTGCTGTGCGCGCTGTGAGATGATGCATGCGACG-A 372  
Db 559 GGGCCNCAAGAACTTTTGGGTGNTCCCTGNTGNGCCCGGAGAGTGATGANNATNGCAGCAA 500  
QY 373 CCCCCTACGACATGACCGCTTGTGGCGTGA--TCTTCCGCGCAGCGCGCGCAGTCCG 430  
Db 499 CCCGNNAGACATGAGCCGCTTTTGGGNGNTTTTGGGGCCAGCCCGACAGTCTG 440  
QY 431 ACCTCATGATGTGGCCGACACTCACCAAGATGAGCCCGACGCTTGCAGAGTCT 490  
Db 439 A-GTNAATGATGTGGGNGNANNTAACCAAAAGAGGCCAGNG-TTTCGAAGTTT 382  
QY 491 AGCAGCAGATGCCGAGCGCGCTACGTGTCTCCATGGGAGACTGCGCAACGAGAG 550  
Db 381 AAGACCAAGATGCCGAGCGCGCANAAAGTGTTCANGGGGAG-TGNGCCAAAGNGNG 323  
QY 551 GCTACTACACTATTCCTACTGCTGTGAGGAGGCTGCGACCGCATCGTCCGTGACA 610  
Db 322 GGTAAACCACTATTCCTAATNGGTGTAGGGGNTGCCACTTGTGCCCGGAGAA 263  
QY 611 TCTACATCCAGGCTGCCCACTACGCGCGAGCCCTGTCTACGCGCATCTGACGCTGC 670  
Db 262 TTNAATCCAGGCTGCCCAACNANGCGAGGCCCTGTTTTANGCATCTGACGCTGC 203  
QY 671 AAGAGAAATCAAGCGGAGCGGAGCTGCANATTTGGTACCGCAGGTAGGGCCGCC 730  
Db 202 AAGAGAAATCAAGCGGAGCGGAGCTGCANATTTGGTACCGCAGGTAGGGCCGCC 143  
QY 731 GCCGCGCGGAGCGCTGTGCGCGCTGCTGCCAGCGCTGTGTCCCGTAGAGTTGTC 790  
Db 142 GCCGCGCGGAGCGCTGTGCGCGCTGCTGCCAGCGCTGTGTGTCCCGTAGAGTTGTC 83  
QY 791 AATAAAGCTGCGCTGCGGCAAAAAA 824  
Db 82 AATAAAGCTGCGCTGCGGCAAAAAA 49

RESULT 6  
US-09-232-149A-32/c  
; Sequence 32, Application US/09232149A  
; Patent No. 6465611  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, David C.  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
; FILE REFERENCE: 210121.427C6  
; CURRENT APPLICATION NUMBER: US/09/232.149A  
; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(789)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-232-149A-32

Query Match 46.7%; Score 384.6; DB 3; Length 789;  
Best Local Similarity 75.9%; Pred. No. 4.2e-80;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;  
QY 141 GGGCGCGCTGTGACGACGAGGTGTCCATCAGAGCGTGCCACCGATGCGCCAAAGCAG 200  
Db 739 GGGGAGATGTGNNAGANGNGTTTCTTAGAGNNGGGCCACCGGGGCCCGAAGGG 680  
QY 201 CACCCAGCTGCTGTGCAAGGCGAGCGTGCTCCAAACCGACGCGGGCGCA 260

Db 679 GGANCCANCTTGGCCNNCCAAAGGCGTGGGTTCCCAAACCAAGNANCG369GA 620  
Qy 261 GTATGTGTGGCCCAAGCTGATGACTCTGCT---CACTGGGCGCGCGAGTTCTCTGTG 317  
Db 619 GGATTTGGGGCCAAAGGGGGATGACTTTGTGAAACTGGGNCCTCCCGAGANTTTTGTGN 560  
Qy 318 G---CCCATGACCTTGGGCTGGCTGCTGCTGCGCGTGGAGATGATGACATGCGAG-A 372  
Db 559 GGGGCGNCAAGAACTTTTGGGTGCTGCTGCTGCTGCTGCGCGAGATGATGATGACAGAA 500  
Qy 373 CCCCCTACGACATGAGACCGCTTTGGCGTGG--TCTTCCGCGCAAGCCCGCGCAATGCTCG 430  
Db 499 CCCCNNAAAGACATGAGNCCTGTTTGGGAGNNTTTTGGGCGCAGCCGNGCAGTCTG 440  
Qy 431 ACCTCATGATGCTGGCGCGGACACTCAACCAAGATGGCCCGCTTGCGAAGTCT 490  
Db 439 A-GTNATGATTTGTGCGNGNANNTAATCAAAAGAGGCGCCCAAGNG-TTTGCAAGGTTT 382  
Qy 491 ACACACAGATCCCGAGCCGCGCTACGCTGCTCCATGGAGAGTGCACCAAGGAGAG 550  
Db 381 AAGACACAGATCCCGAGCCGCGAGAAAGTGTTCANAGGAG--TGNGCCAAAGGNGNG 323  
Qy 551 GCTACTACCACTATTTCTACTCGGTGTGAGGGGCTGCGACCGCATGCTCCGTGACA 610  
Db 322 GGTAAACCACTATTTCTAATGAGTGTGAGGGGTCGACCGCATGCTCCGTGAAA 263  
Qy 611 TCTACATCCAGGCTGCCCACTACGCGCGAGGCGCTGCTCAAGGCACTCTGACGTGC 670  
Db 262 TTNAATCCAGGCTGCCCACTAATGAGTGTGAGGGGTCGACCGCATGCTCCGTGAAA 203  
Qy 671 AGAGGAAGATCAACCGGAGCGGAGCTGCAGATCTGTAACGAGATGAGCGCGCGCC 730  
Db 202 AGAGGAANATCAACCGGAGCGGAGCTGCANATTTGTTACGAGATGAGGCGCGCC 143  
Qy 731 GCCCGCGCGGAGCTGTGCGCTGTCTGTCCCAAGCTCTGTTGTCTCCGTGAGTTTC 790  
Db 142 GCCCGCGCGGAGCTGTGCGCTGTCTGTCCCAAGCTGTTGTCTCCGAGAGTTTC 83  
Qy 791 AATAAACCCTGCTCGGCAAAAAA 824  
Db 82 AATAAACCCTGCTCGGCAAAAAA 49

RESULT 7  
US-09-159-812-32/C  
; Sequence 32, Application US/09159812A  
; Patent No. 6613872  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, David C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF  
; FILE REFERENCE: 210121.428C5  
; CURRENT APPLICATION NUMBER: US/09/159, 812A  
; NUMBER OF SEQ ID NOS: 306  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(789)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-159-812-32

Query Match 46.7%; Score 384.6; DB 4; Length 789;  
Best Local Similarity 75.9%; Pred. No. 4,2e-80;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

Qy 141 GGGCCGGCTGTGACGACGAGGTGTCATGAGCGTGGCCACCGATGGCCCAAGCAG 200

141 GGGCCGGCTGTGACGACGAGGTGTCATGAGCGTGGCCACCGATGGCCCAAGCAG 200

Db 739 GGGGATGTGTGNNNAGANGNGTTTTNTTAGANNNGGCCACCGGGGCCGAAAGC 680  
Qy 201 CACCACCTGCTGCTGCGCAAGGCGAGGCGTGGCTCCCAAACCAAGACCGGAGCGA 260  
Db 679 GGANCCANCTTGGCCNNCCAAAGGCGTGGGTTCCCAAACCAAGNANCG699GA 620  
Qy 261 GTATGTGTGGCCCAAGCTGATGACTCTGCT---CACTGGGCGCGCGAGTTCTCTGTG 317  
Db 619 GGATTTGGGGCCAAAGGGGGATGACTTTGTGAAACTGGGNCCTCCCGAGANTTTTGTGN 560  
Qy 318 G---CCCATGACCTTGGGCTGGCTGCTGCTGCGCGTGGAGATGATGACATGCGAG-A 372  
Db 559 GGGGCGNCAAGAACTTTTGGGTGCTGCTGCTGCTGCTGCGCGAGATGATGATGACAGAA 500  
Qy 373 CCCCCTACGACATGAGACCGCTTTGGCGTGG--TCTTCCGCGCAAGCCCGCGCAATGCTCG 430  
Db 499 CCCCNNAAAGACATGAGNCCTGTTTGGGAGNNTTTTGGGCGCAGCCGNGCAGTCTG 440  
Qy 431 ACCTCATGATGCTGGCGCGGACACTCAACCAAGATGGCCCGCTTGCGAAGTCT 490  
Db 439 A-GTNATGATTTGTGCGNGNANNTAATCAAAAGAGGCGCCCAAGNG-TTTGCAAGGTTT 382  
Qy 491 ACACACAGATCCCGAGCCGCGCTACGCTGCTCCATGGAGAGTGCACCAAGGAGAG 550  
Db 381 AAGACACAGATCCCGAGCCGCGAGAAAGTGTTCANAGGAG--TGNGCCAAAGGNGNG 323  
Qy 551 GCTACTACCACTATTTCTACTCGGTGTGAGGGGCTGCGACCGCATGCTCCGTGACA 610  
Db 322 GGTAAACCACTATTTCTAATGAGTGTGAGGGGTCGACCGCATGCTCCGTGAAA 263  
Qy 611 TCTACATCCAGGCTGCCCACTACGCGCGAGGCGCTGCTCAAGGCACTCTGACGTGC 670  
Db 262 TTNAATCCAGGCTGCCCACTAATGAGTGTGAGGGGTCGACCGCATGCTCCGTGAAA 203  
Qy 671 AGAGGAAGATCAACCGGAGCGGAGCTGCAGATCTGTTACGAGATGAGCGCGCGCC 730  
Db 202 AGAGGAANATCAACCGGAGCGGAGCTGCANATTTGTTACGAGATGAGGCGCGCC 143  
Qy 731 GCCCGCGCGGAGCTGTGCGCTGTCTGTCCCAAGCTCTGTTGTCTCCGTGAGTTTC 790  
Db 142 GCCCGCGCGGAGCTGTGCGCTGTCTGTCCCAAGCTGTTGTCTCCGAGAGTTTC 83  
Qy 791 AATAAACCCTGCTCGGCAAAAAA 824  
Db 82 AATAAACCCTGCTCGGCAAAAAA 49

RESULT 8  
US-09-636-215-32/C  
; Sequence 32, Application US/09636215  
; Patent No. 6620822  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, David C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.42717C17  
; CURRENT APPLICATION NUMBER: US/09/636, 215

US-09-636-215-32/C  
; Sequence 32, Application US/09636215  
; Patent No. 6620822  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, David C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.42717C17  
; CURRENT APPLICATION NUMBER: US/09/636, 215

US-09-636-215-32/C  
; Sequence 32, Application US/09636215  
; Patent No. 6620822  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, David C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.42717C17  
; CURRENT APPLICATION NUMBER: US/09/636, 215

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; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-636-215-32

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Query Match      46.7%; Score 384.6; DB 4; Length 789;
Best Local Similarity 75.9%; Pred. No. 4.2e-80;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

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QY 141 GGGCCCGGTGTGACGACGAGGCTGTCCATCAGAGCGTCCACCGATGGCCCAAGCAG 200
DB 739 GGGGAGTGTGNNAGANGGTTTCTTCTAGAGNNGGGCCACCGGGGCGCCGAAGG 680
QY 201 CACCCAGCCTGCTGCCCAAGGCGGAGCGGCTGCCAAACCCAGACCGCGGGGGA 260
DB 679 GGANCACTTGTCCNNCCAAAGNNAGAGCGTGGGTTCCAAACCCAGNANCGGGGGA 620
QY 261 GTATGTGTGCGCAAGCTGATGACCTGT---CAACTGGGCGCGCCGAGTTCTGTG 317
DB 619 GGATTTGGGGGCGAAGGGGATGACTTTGTGAACCTGGAGCCCGGAGNTTTTTGN 560
QY 318 G----CCCATGACCTTGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 372
DB 559 GGGCCNCAAGAACCTTTGGTTGCTGTGNTGNGCCGAGAGTATGNAATNCGACAA 500
QY 373 CCGCGCTACGACATGACCGCTTTGGCGTGG--TCTTCCGCGCCAGCCCGCGCATCGG 430
DB 499 CCGCGNNAAGACATGAGCCGTTTGGGNGNTTTTTGGGGCCAGCCCGGCGCATCTG 440
QY 431 ACGTCATGATGCTGGCGCGCACTACCAACAAAGTGGCCCGCGCTTGCAGAGTCT 490
DB 439 A-GTATGATTTGTGCGNGNANNTAACAAGAGGCGCCGAGNG--TTTGCAGAGTTT 382
QY 491 ACGACAGATGCGGAGCGCGCTACCGTGTCTCATGGGGAGCTGGGCCAAACGAGAG 550
DB 381 AAGACAGATGCGGAGCGCGCAAGAGTGTTCANAGGGAG--TNGCCAAACGAGNG 323
QY 551 GCTACTACCACTATTCTTACTCGGTGTGAGGGGCTGCAACCGCATGTGCGCGTGA 610
DB 322 GGTAAACCACTATTCTTAATNGTGTGAGGGGAGTGGACCGCATTTGCGCGTGA 263
QY 611 TCTACATCCCAAGGCTGCGCACTACCGCCGAGCGCTGCTCTAGGCACTCTGAGCTGC 670
DB 262 TTNAATTCAGAGGTGCGCAACNAGGCCAGAGCGCTGTATTAGGCACTCTGAGCTGC 203
QY 671 AGAGGAAGATCAAGCGGAGCGAGGCTGAGACTGTGTAACCGAGGTAGCGCGCGCC 730
DB 202 AGAGGAANATCAAGCGGAGCGAGGCTGCAATTTGTGTAACCGAGGTAGCGCGCC 143
QY 731 GCGCGCGCGGAGGCTGTGCGCTGCTGTGCTCCAGCGCTGTGTGTCGCGTGA 790
DB 142 GCGCGCGCGGAGGCTGTGCGCTGCTGTGCTCCAGCGCTGTGTGTCGCGTGA 83
QY 791 AATTAACCTGCGCTGCGGCAAAAAA 824
DB 82 AATTAACCTGCGCTGCGGCAAAAAA 49

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RESULT 9
US-09-685-166A-32/c
; Sequence 32, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.

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; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-685-166A-32

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Query Match      46.7%; Score 384.6; DB 4; Length 789;
Best Local Similarity 75.9%; Pred. No. 4.2e-80;
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

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QY 141 GGGCCCGGTGTGACGACGAGGCTGTCCATCAGAGCGTCCACCGATGGCCCAAGCAG 200
DB 739 GGGGAGTGTGNNAGANGGTTTCTTCTAGAGNNGGGCCACCGGGGCGCCGAAGG 680
QY 201 CACCCAGCCTGCTGCCCAAGGCGGAGCGGCTGCCAAACCCAGACCGCGGGGGA 260
DB 679 GGANCACTTGTCCNNCCAAAGNNAGAGCGTGGGTTCCAAACCCAGNANCGGGGGA 620
QY 261 GTATGTGTGCGCAAGCTGATGACCTGT---CAACTGGGCGCGCCGAGTTCTGTG 317
DB 619 GGATTTGGGGGCGAAGGGGATGACTTTGTGAACCTGGAGCCCGGAGNTTTTTGN 560
QY 318 G----CCCATGACCTTGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 372
DB 559 GGGCCNCAAGAACCTTTGGTTGCTGTGNTGNGCCGAGAGTATGNAATNCGACAA 500
QY 373 CCGCGCTACGACATGACCGCTTTGGCGTGG--TCTTCCGCGCCAGCCCGCGCATCGG 430
DB 499 CCGCGNNAAGACATGAGCCGTTTGGGNGNTTTTTGGGGCCAGCCCGGCGCATCTG 440
QY 431 ACGTCATGATGCTGGCGCGCACTACCAACAAAGATGGCCCGCGCTTGCAGAGTCT 490
DB 439 A-GTATGATTTGTGCGNGNANNTAACAAGAGAGGCGCCGAGNG--TTTGCAGAGTTT 382
QY 491 ACGACAGATGCGGAGCGCGCTACCGTGTCTCATGGGGAGTGGCCAAACGAGAG 550
DB 381 AAGACAGATGCGGAGCGCGGAGGCTTCCANAGGGAG--TNGCCAAACGAGNG 323
QY 551 GCTACTACCACTATTCTTACTCGGTGTGAGGGGCTGCAACCGCATTTGCGCGTGA 610
DB 322 GGTAAACCACTATTCTTAATNGTGTGAGGGGAGTGGACCGCATTTGCGCGTGA 263
QY 611 TCTACATCCCAAGGCTGCGCACTACCGCGGCGCTGCTCTAGGCACTCTGAGCTGC 670
DB 262 TTNAATTCAGAGGTGCGCAACNAGGCCAGAGCGCTGTATTAGGCACTCTGAGCTGC 203
QY 671 AGAGGAAGATCAAGCGGAGCGAGGCTGCAATCTGTGTACCGAGGTAGCGCGCGCC 730

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Db 202 AGAGAAATCAACGGGAGCGAGGCTGCANATTGTGATCCGAGTAGGGCCGCC 143  
Qy 731 GCCGCCCGGAGGCTGCGCGCTGTCCCGAGCCCTGTGTGTC 790  
Db 142 GCCGCCCGGAGGCTGTGCGCTGTCCCGAGCCGTGTTGTCTCCGAGAGTTGTC 83  
Qy 791 AATTAACCTGCTCGGCGCAAAAAAAAAA 824  
Db 82 AATTAACCTGCTCGGCGCAAAAAAAAAA 49

RESULT 10  
US-09-115-453-32/c  
; Sequence 32, Application US/09115453B  
; Patent No. 6657056  
; GENERAL INFORMATION:  
; APPLICANT: Xu, JIANGCHUN  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND  
; FILE REFERENCE: 210121.427C4  
; CURRENT APPLICATION NUMBER: US/09/115.453B  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1) ... (789)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-115-453-32

Query Match 46.7%; Score 384.6; DB 4; Length 789;  
Best Local Similarity 75.9%; Pred. No. 4.2e-80;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

Qy 141 GGGCCCCGCTGTGACGACAGAGTGTCCATCAAGCTGCGCACCGATGCGCCCAAGCAG 200  
Db 739 GGGGAGATGTGNNNAGANGNGTTCNTTGAAGNNGGGCCACCGGCGCGCAAGGG 680  
Qy 201 CACCCAGCTGCGCTGCGCAAGGCGCAGCGGTGCTCCCAACCCAGCCGCGGGGGA 260  
Db 679 GGANCCANCTTGCCNNCCAAAGNAGAGCGCTGGGTTCCAAACCCAGNANCCGGGGGA 620  
Qy 261 GTATGTGTGCGCAAGCTGATGACTCTGT--CAACTGGGCGCGCGAGTTCTGTG 317  
Db 619 GGATTTGGGGCGCAAGGGGATGACTTTGTGAACCTGGGNCCTCCCGAGNTTTTGN 560  
Qy 318 G----CCCATGACCTTGCGCTGCGCTGCTGCGCGCTGAGATGATGCAATGCGAGC-A 372  
Db 559 GGGGCNCAAGAACTTTTGGGTTGNCCTGNTGNCCTCGGAGAGTATGNAATNCCAGCAA 500  
Qy 373 CCGCGCTACGACGATGACCGCTTTGGCGTG--TCTTCCGGCGCAGCCCGGCGCAGTCCG 430  
Db 499 CCGCGNNAAGACATGNCCTGTTTGGGNGNTTTTGGGGCCAGCCCGGCGCAGTCTG 440  
Qy 431 ACCTCATGATCGTGGCGCGCACTCACTCAACAAGATGCGCCAGCGCTTGGCAAGTCT 490  
Db 439 A-GTNATGATTTGTGGCGNANANTTAACAAAGAGGGCCCAAGNG-TTTGCAAGGTTT 382  
Qy 491 ACGACCAAGATCCCGAGCGCGCTACGTTGCTCCATGGGAGCTGCGCAACGAGAG 550  
Db 381 AAGACCAAGATCCCGAGCGCGAGCAAGAGTGTTCANAGGGAG-TGNCCTCAACGAGNG 323  
Qy 551 GCTACTACCACTATTTCTACTCGGTGAGGGGTGCGACGATGCTGCGCGGAGCA 610  
Db 322 GGTAAACCACTATTTCTTAATNGGTGTGAGGGGTGCGACGCACTGTGTGCGCGGAAA 263  
Qy 611 TCTACATCCAGGCTGCGCACTACGCGCGAGGCTGCTCAAGGCATCTCTGAGCTGC 670

Db 262 TTNAATCCAGGGTGCACCAACNAGCCGAGCCCTGTTTANAGGATCCTGAGCTGC 203  
Qy 671 AGAGAAATCAACGGGAGCGAGGCTGCAATCTGTACCCGAGTAGGGCCGCC 730  
Db 202 AGAGAAATCAACGGGAGCGAGGCTGCANATTGTGATCCGAGTAGGGCCGCC 143  
Qy 731 GCCGCCCGGAGGCTGCGCGCTGTCCCGAGCCCTGTGTGTC 790  
Db 142 GCCGCCCGGAGGCTGTGCGCTGTCCCGAGCCGTGTTGTCTCCGAGAGTTGTC 83  
Qy 791 AATTAACCTGCTCGGCGCAAAAAAAAAA 824  
Db 82 AATTAACCTGCTCGGCGCAAAAAAAAAA 49

RESULT 11  
US-09-688-489-32/c  
; Sequence 32, Application US/09688489  
; Patent No. 6664377  
; GENERAL INFORMATION:  
; APPLICANT: Xu, JIANGCHUN  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
; FILE REFERENCE: 210121.427D2  
; CURRENT APPLICATION NUMBER: US/09/688.489  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 789  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1) ... (789)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-688-489-32

Query Match 46.7%; Score 384.6; DB 4; Length 789;  
Best Local Similarity 75.9%; Pred. No. 4.2e-80;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

Qy 141 GGGCCCCGCTGTGACGACAGAGTGTCCATCAAGCTGCGCACCGATGCGCCCAAGCAG 200  
Db 739 GGGGAGATGTGNNNAGANGNGTTCNTTGAAGNNGGGCCACCGGCGCGCAAGGG 680  
Qy 201 CACCCAGCTGCGCTGCGCAAGGCGCAGCGGTGCTCCCAACCCAGCCGCGGGGGA 260  
Db 679 GGANCCANCTTGCCNNCCAAAGNAGAGCGCTGGGTTCCAAACCCAGNANCCGGGGGA 620  
Qy 261 GTATGTGTGCGCAAGCTGATGACTCTGT--CAACTGGGCGCGCGAGTTCTGTG 317  
Db 619 GGATTTGGGGCGCAAGGGGATGACTTTGTGAACCTGGGNCCTCCCGAGNTTTTGN 560  
Qy 318 G----CCCATGACCTTGCGCTGCGCTGCTGCGCGCTGAGATGATGCAATGCGAGC-A 372  
Db 559 GGGGCNCAAGAACTTTTGGGTTGNCCTGNTGNCCTCGGAGAGTATGNAATNCCAGCAA 500  
Qy 373 CCGCGCTACGACGATGACCGCTTTGGCGTG--TCTTCCGGCGCAGCCCGGCGCAGTCCG 430  
Db 499 CCGCGNNAAGACATGNCCTGTTTGGGNGNTTTTGGGGCCAGCCCGGCGCAGTCTG 440  
Qy 431 ACCTCATGATCGTGGCGCGCACTCACTCAACAAGATGCGCCAGCGCTTGGCAAGTCT 490  
Db 439 A-GTNATGATTTGTGGCGNANANTTAACAAAGAGGGCCCAAGNG-TTTGCAAGGTTT 382  
Qy 491 ACGACCAAGATCCCGAGCGCGCTACGTTGCTCCATGGGAGCTGCGCAACGAGAG 550  
Db 381 AAGACCAAGATCCCGAGCGCGAGCAAGAGTGTTCANAGGGAG-TGNCCTCAACGAGNG 323

QY 551 GCTACTACCACTATTCCTACTCGGTGTGAGGGGCTGCGACCGCATCGTACCCTGTGACA 610  
 Db 322 GGTAAACCACTATTCTTAATGATGTGAGGGGATGCGACCGCATTTGTGCCGTGAGAAA 263  
 QY 611 TCTACATCCGAGGCTGCCACCTACCGCGCGAGCCCTGCTCTACGGCCATTCCTGACCTGC 670  
 Db 262 TTNAATATCCAGAGGTGCCACCNANAGCCGAGGCCCTGTTTANAGCATCTGACAGCTGC 203  
 QY 671 AGAGGAAGATCAAGCCGAGCGGAGGAGGTGAGATCTGTACCGCAGATAGCCGCGCGCC 730  
 Db 202 AGAGGAAGATCAAGCCGAGCGGAGGAGGTGAGATCTGTACCGCAGATAGCCGCGCGCC 143  
 QY 731 GCCCGCCGCGAGGCTGTGCGCGCTGCTGTCCCAAGCTGCTGTGTCTCCGTAGAGTTGTC 790  
 Db 142 GCCCGCCGCGAGGCTGTGCGCGCTGCTGTCCCAAGCTGCTGTGTCTCCGTAGAGTTGTC 83  
 QY 791 AATTAACCTGCTCCGCGGCAAAAAA 824  
 Db 82 AATTAACCTGCTCCGCGGCAAAAAA 49

## RESULT 12

US-09-679-426-32/C  
 ; Sequence 32, Application US/09679426  
 ; Patent No. 6759515

## GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: Harlocker, Susan L.  
 APPLICANT: Jiang, Yuqi  
 APPLICANT: Henderson, Robert A.  
 APPLICANT: Kalos, Michael D.  
 APPLICANT: Fanger, Gary R.  
 APPLICANT: Retter, Marc W.  
 APPLICANT: Stolk, John A.  
 APPLICANT: Day, Craig H.  
 APPLICANT: Vedvick, Thomas S.  
 APPLICANT: Carter, Darrick  
 APPLICANT: Li, Samuel  
 APPLICANT: Wang, Aijun  
 APPLICANT: Skeiky, Yasir A.W.  
 APPLICANT: Hepler, William  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 FILE REFERENCE: 210121.427C20  
 CURRENT APPLICATION NUMBER: US/09/679,426  
 CURRENT FILING DATE: 2000-10-02  
 NUMBER OF SEQ ID NOS: 895  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 32  
 LENGTH: 789  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1).. (789)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-679-426-32

Query Match 46.7%; Score 384.6; DB 4; Length 789;  
 Best Local Similarity 75.9%; Pred. No. 4.2e-80;  
 Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;  
 QY 141 GGGCCCCGCTGTGCAGCAAGGTGTCATCAGAGGTGGCCACCGATG3CCCAAGCAG 200  
 Db 739 GGGGAGATGTGANNAGANGANGTTTCTTAAAGNNGGCCCAACGGGGGCCGGAAGG 680  
 QY 201 CACCCAGCTGCTCCCTGCAAGAGCCGAGGCTGCCAAACCAAGCAGCCGCGGCGA 260  
 Db 679 GGANCAACCTTGCCTCCNNAAGAGGCGTGGGTCCCAAAACCGANANAGGGGGGA 620  
 QY 261 GATGTGTGGCCAGCTGATGACTCGT---CACTGGGCGCGCGAGTTCTCTGTG 317

Db 619 GGATTTGGGGGCCAAGGGGATGACTTTGTGAACATGGNCCCGCGGAGNTTTTGTN 560  
 QY 318 G-----CCATGACTTTGGGCTGTGCTGCTGCGCGCGGAGATGATGATGACAGC-A 372  
 Db 559 GGGCCNCAAGAACTTTTGGGTGATGCTGNTGNGCCCGGAGGTGATNANAATNGACGAA 500  
 QY 373 CCGCGCTGCGCATGAGACCGCTTGGCGTG3--TCTTCCGCGCAGCCCGCGCACTGC 430  
 Db 499 CCGCANNAGACATGACCGGTTTGGGAGNNTTTTGGGGCCAGCCCGGCGCATGCTG 440  
 QY 431 ACGTCATGATGTGCGCGGCACTACACCAAGATGCCCCGAGCGCTTCCGAAGGTCT 490  
 Db 439 A-GTATGATTTGTGCMNGNANNTAACAAGAGAGGCCCAAGG-TTGCAAGGTTT 382  
 QY 491 ACGACCAATGCGCGAGCGGCTACGAGTCTCCATGAGGAGTGTGCGCAAGAGAG 550  
 Db 381 AAGACCAATGCGCGAGCGGCTACGAGTCTCCATGAGGAGTGTGCGCAAGAGAG 323  
 QY 551 GCTACTACCACTATTCCTACTCGGTGTGAGGGGCTGCGACCGCATCTGAGAGCTGC 610  
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 QY 611 TCTACATCCGAGGCTGCCACCTACGCGCGAGGCTGCTCTACGCGCATCTGAGAGCTGC 670  
 Db 262 TTNAATATCCAGAGGTGCCACCNANAGCCGAGGCCCTGTTTANAGCATCTGAGAGCTGC 203  
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 Db 202 AGAGGAAGATCAAGCGGAGCGGAGGCTGACANATTTGTATCCGAGTAGGCGCCGCC 143  
 QY 731 GCCCGCCGCGAGGCTGTGCGCGCTGCTGTCCCAAGCTGCTGTGTCTCCGTAGAGTTGTC 790  
 Db 142 GCCCGCCGCGAGGCTGTGCGCGCTGCTGTCCCAAGCTGCTGTGTCTCCGTAGAGTTGTC 83  
 QY 791 AATTAACCTGCTCCGCGCAAAAAA 824  
 Db 82 AATTAACCTGCTCCGCGCAAAAAA 49

## RESULT 13

US-09-759-143-32/C  
 ; Sequence 32, Application US/09759143  
 ; Patent No. 6800746

## GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: Harlocker, Susan L.  
 APPLICANT: Jiang, Yuqi  
 APPLICANT: Henderson, Robert A.  
 APPLICANT: Kalos, Michael D.  
 APPLICANT: Fanger, Gary R.  
 APPLICANT: Retter, Marc W.  
 APPLICANT: Stolk, John A.  
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 APPLICANT: Carter, Darrick  
 APPLICANT: Li, Samuel  
 APPLICANT: Wang, Aijun  
 APPLICANT: Skeiky, Yasir A.W.  
 APPLICANT: Hepler, William  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 FILE REFERENCE: 210121.427C23  
 CURRENT APPLICATION NUMBER: US/09/759,143  
 CURRENT FILING DATE: 2001-01-12  
 NUMBER OF SEQ ID NOS: 934  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 32  
 LENGTH: 789  
 TYPE: DNA  
 ORGANISM: Homo sapien

FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(789)  
OTHER INFORMATION: n = A,T,C or G  
US-09-759-143-32

Query Match 46.7%; Score 384.6; DB 4; Length 789;  
Best Local Similarity 75.9%; Pred. No. 4.2e-80;  
Matches 527; Conservative 0; Mismatches 154; Indels 13; Gaps 7;

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QY 141 GGGCCCCGCTGTGACGACAGAGTGTCCATCAGAGGTGGCCACCGATGGCCCAAGCAG 200
DB 739 GGGGGATGTGTGNNNAGANNNGNTTTTNTTAGANNNGGCCACCGGGGCCCGAAGGG 680
QY 201 CACCCAGCTGCGCTGGCCAAAGGCGAGCGGTGCTCCCAACCCAGCGCGGGCGA 260
DB 679 GGANCCANCTTGGCCNNCCAAAGNNAAGAGCGTGGGTTCCCAACCCAGNNAACGGGGGA 620
QY 261 GTATGTGTGGCCAAAGCTGTGATGACTGT---CAACTGGGCGCGCGAGTTCTGTG 317
DB 619 GGATTTGGGGGCCAAAGGGGATGACTTTGTGAACAGGGGCCCGCGAGNTTTTGN 560
QY 318 G---CCCATGACCTTGGCGCTGCTGTGCGCGCTGGAGATGATGACATGGCAGC-A 372
DB 559 GGGCCNCAAGAACTTTTGGTTGNCCTGNTGNCCTGGAGGTGATGANAATNGCAGCAA 500
QY 373 CCCCCTACGACATGACCGGCTTTGGGGTGG--TCTTCCGCGCAGGCGCGGCAAGTCCG 430
DB 499 CCCCNNNAAGCATGAGNCGGGTTTGGGNGNTTTTGGGGCCAGCCCGNCCAGTCTG 440
QY 431 ACCTGATGATGTGGCCGCGCACACTCAACAAGATGGCCCGCTTGGCAAGTCT 490
DB 439 A-GTNAATGATTTGGCGNANNANNTAAACAAAGAGGGGCCCAAG--TTTGGCAAGTTT 382
QY 491 ACGACCATGATGCGGAGCGCGCTACGTGTCTTCATGGGAGCTGGCCCAAGAGAG 550
DB 381 AAGCCAGATGCGGAGCGCGGAGAGGTGTTCCANGGGAG--TGNGCCAAACGNGNG 323
QY 551 GCTACTACACTATTCTACTCGGTGTGAGGGGCTGGACCGCATGTGTGCGGTGACA 610
DB 322 GGTAAACCACTATTCTTAATNGGTGTGAGGGGNTGGACCGCATGTGTGCGGTGAAA 263
QY 611 TCTACATCCAGAGCTGCGCACTACGCGCGAGGCGCTGTCTACGGCATCTGAGCTGC 670
DB 262 TTNAATATCCAGAGGTGCGCACANAGGCCAGGCGCTGTGTANGGCATCTGAGAGCTGC 203
QY 671 AGAGGAAGATCAAGCGGAGCGGAGGCTGCAGATCTGTGATCCGAGGTAGCGCGCGC 730
DB 202 AGAGGAATCAAGCGGAGCGGAGGCTGCANATTTGTATCCGAGGTAGGGCGCGCC 143
QY 731 GCGCGCGCGGAGGCTGTGCGCGCTGTGCTCCCAAGCTGTGTGTCCCGTGAAGTTGTC 790
DB 142 GCGCGCGCGGAGGCTGTGCGCGCTGTGCTCCCAAGCTGTGTGTCCCGTGAAGTTGTC 83
QY 791 AATTAACCTGCGCTCGGCAAAAAAAAAAAAA 824
DB 82 AATTAACCTGCGCTCGGCAAAAAAAAAAAAA 49
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RESULT 14  
US-09-651-236-32/c  
Sequence 32, Application US/09651236  
Patent No. 6818751

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yungui  
APPLICANT: Henderson, Robert A.  
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APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER  
FILE REFERENCE: 210121.42718C18  
CURRENT FILING DATE: US/09/651.236  
NUMBER OF SEQ ID NOS: 865  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 789  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(789)  
OTHER INFORMATION: n = A,T,C or G  
US-09-651-236-32

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DB 679 GGANCCANCTTGGCCNNCCAAAGNNAAGAGCGTGGGTTCCCAACCCAGNNAACGGGGGA 620
QY 261 GTATGTGTGGCCAAAGCTGTGATGACTGT---CAACTGGGCGCGCGAGTTCTGTG 317
DB 619 GGATTTGGGGGCCAAAGGGGATGACTTTGTGAACAGGGGCCCGCGAGNTTTTGN 560
QY 318 G---CCCATGACCTTGGCGCTGCTGTGCGCGCTGGAGATGATGACATGGCAGC-A 372
DB 559 GGGCCNCAAGAACTTTTGGGTGNCCTGNTGNCCTGGAGGTGATGANAATNGCAGCAA 500
QY 551 GCTACTACACTATTCTACTCGGTGTGAGGGGCTGGACCGCATGTGTGCGGTGACA 610
DB 322 GGTAAACCACTATTCTTAATNGGTGTGAGGGGNTGGACCGCATGTGTGCGGTGAAA 263
QY 611 TCTACATCCAGAGCTGCGCACTACGCGCGAGGCGCTGTCTACGGCATCTGAGCTGC 670
DB 262 TTNAATATCCAGAGGTGCGCACANAGGCCAGGCGCTGTGTANGGCATCTGAGAGCTGC 203
QY 671 AGAGGAAGATCAAGCGGAGCGGAGGCTGCAGATCTGTGATCCGAGGTAGCGCGCGC 730
DB 202 AGAGGAATCAAGCGGAGCGGAGGCTGCANATTTGTATCCGAGGTAGGGCGCGCC 143
QY 731 GCGCGCGCGGAGGCTGTGCGCGCTGTGCTCCCAAGCTGTGTGTCCCGTGAAGTTGTC 790
DB 142 GCGCGCGCGGAGGCTGTGCGCGCTGTGCTCCCAAGCTGTGTGTCCCGTGAAGTTGTC 83
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